

From: Bunner, Bridget
Sent: Friday, August 02, 2002 4:31 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

10/10/2000

10/12/1999

09/721,341

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

RECEIVED
AUG - 2 2003
STIC

8/6 Note: consider making 103
if App. overcomes 112-1

1031, 1050

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/6
Date Completed: 8/7
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.):
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: as
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 18:04:30 ; Search time 13.09 seconds
(without alignments)
653.091 Million cell updates/sec

Title: us-09-686-020a-2

Perfect score: 1819

Sequence: 1 MALEQNQSTDYVEENEMNG.....VEEFPDSEGTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1620	99.1	350	2	US-08-966-316-18
3	659	36.2	358	1	US-08-153-848-19
4	659	36.2	358	3	US-09-299-843A-19
5	659	36.2	358	4	US-09-088-337B-19
6	659	36.2	358	5	PCT-US93-11153-19
7	659	36.2	378	1	US-08-153-848-15
8	659	36.2	378	3	US-09-299-843A-15
9	659	36.2	378	4	US-09-251-545-1
10	659	36.2	378	4	US-09-088-337B-15
11	659	36.2	378	5	PCT-US93-11153-15
12	659	36.2	410	1	US-08-153-848-7
13	659	36.2	410	3	US-09-299-843A-7
14	659	36.2	410	4	US-09-088-337B-7
15	659	36.2	410	5	PCT-US93-11153-7
16	650	35.7	378	3	US-09-299-843A-66
17	650	35.7	378	4	US-09-088-337B-66
18	643	35.3	378	1	US-08-383-750-2
19	643	35.3	378	3	US-08-383-751A-2
20	643	35.3	378	3	US-08-352-678-2
21	643	35.3	378	4	US-09-045-583-49
22	643	35.3	378	5	PCT-US93-09636-2
23	637	35.0	357	4	US-09-266-464-2
24	635.5	34.9	359	1	US-08-153-848-24
25	635.5	34.9	359	3	US-09-299-843A-24
26	635.5	34.9	359	4	US-09-088-337B-24
27	635.5	34.9	359	5	PCT-US93-11153-24

28 606.5 33.3 361 2 US-08-902-294-2 Sequence 2, Appli
29 606.5 33.3 361 3 US-09-178-637-2 Sequence 2, Appli
30 583 32.1 374 4 US-09-045-583-48 Sequence 48, Appli
31 581 31.9 342 4 US-09-116-498-4 Sequence 4, Appli
32 569 31.3 342 2 US-09-116-498-6 Sequence 6, Appli
33 560 30.8 342 2 US-08-742-011-2 Sequence 2, Appli
34 560 30.8 342 4 US-09-275-384B-5 Sequence 5, Appli
35 560 30.8 342 4 US-09-116-498-2 Sequence 2, Appli
36 560 30.8 342 4 US-09-449-437A-2 Sequence 2, Appli
37 537.5 29.5 360 4 US-08-875-573-20 Sequence 20, Appli
38 537.5 29.5 360 4 US-09-232-878-2 Sequence 2, Appli
39 537.5 29.5 360 4 US-09-045-583-55 Sequence 55, Appli
40 534.5 29.4 355 1 US-07-759-568-1 Sequence 1, Appli
41 534.5 29.4 355 1 US-08-450-393A-8 Sequence 8, Appli
42 534.5 29.4 355 2 US-08-390-000A-5 Sequence 5, Appli
43 534.5 29.4 355 4 US-08-446-669-8 Sequence 8, Appli
44 534.5 29.4 355 5 PCT-US95-00476-8 Sequence 8, Appli
45 534.5 29.4 360 1 US-08-202-056-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-966-316-16
; Sequence 16, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; STRANDEDNESS: single
; IMMEDIATE SOURCE:
; LIBRARY: UTRSNOT11
; CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 7.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYEEENEMNGTYDYSOYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60
DB 1 MALEONQSTDYEEENEMNGTYDYSOYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60
QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKCKITSALYT 120
DB 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKCKITSALYT 120
QY 121 LNFVSGMQLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 LNFVSGMQLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
QY 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSLNLP 300
DB 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSLNLP 300
QY 301 ILYVFMGASFKNYVMKAKYKGSRRQRQSVVEEPPFDSGTEPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKAKYKGSRRQRQSVVEEPPFDSGTEPTSTFSI 350

RESULT 2

US-08-966-316-18
Sequence 18, Application US/08966316
Patent No. 5932445

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murry, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 7.1e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONQSTDYEEENEMNGTYDYSOYELICIKEDVREFAKVFPLVFTIVFVIGLAGNS 60
DB 1 MAVEYNQSTDYEEENEMNDTHDYSOYEVICIKKEVRKFAKVFPAFFIAFIIGLAGNS 60
QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKCKITSALYT 120
DB 61 TVVAIYAYKKRRTKTDVYILNLAVADLLLTLPFWAVNAVHGVWLGKMKCKITSALYT 120
QY 121 LNFVSGMQLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
DB 121 VNFVSGMQLACISIDRYAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVNH 180
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
DB 181 KARCVPFIIPYHLGTSMKASIQLEICIGFIIPFLMVCYFITAKTLKMPNIIKISRPLK 240
QY 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSLNLP 300
DB 241 VLLTWVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSLNLP 300
QY 301 ILYVFMGASFKNYVMKAKYKGSRRQRQSVVEEPPFDSGTEPTSTFSI 350
DB 301 VLYVFMGTSTFKNYIMKAKYKGSRRQRQSVVEEPPFDSGTEPTSTFSI 350

RESULT 3

US-08-153-848-19
Sequence 19, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

```

; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 36.2%; Score 659; DB 1; Length 358;
Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSQSDYYEENMGTYDYSOYELICIKEDYREFAKVFLPVLTVFVIGLAGNS 60
DB 1 VCLQDEVTDYIGDNT---TVDYTLFESLCKSKDVRNFKAWFLPIMYSIICFVGLLNG 57

QY 61 MVVAIYAYKKQRTDVTYILNLAVALDILLFTLPFWAVNAVHGVGLKIMCKITSALYT 120
DB 58 LVVLTYYIKRLKTMDDTYLLNLAVALDILLFTLPFWAYSAKSWGVHFCFLIFAIYK 117

QY 121 LNFVSGMQLACISIDRYVAVTKVPS-----QSGVGKPCWIIICFCVWMAILLISIPQLVY 176
DB 118 MSFFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPPELLYS 177

QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVVPFLMGVCVFITARTLMKMP 231
DB 178 DLORSSSQAMRCSLITEH---VEAFITQVAQWVIGLVPFLANSFCYLVIIIRLLQAR 234

QY 232 NIKISRLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESTI 291
DB 235 NFERNKAIRKIIAVVVFIVFQLPYNGVLAQTVANFNITSSTCELSKQLNIAYDVYSL 294

QY 292 ALFHSCNLPILYVFMGASFKNVYKAKYG-----SW-----RRQRSVEEFPFD 337
DB 295 ACVRCVNPFLYAFIGVFRNDLFLKFDGLCLSQELQRMSSCRHRRSSMSVE----- 349

QY 338 SEGPTPTSTFS 349
DB 350 ---AETTTTFS 357

RESULT 5
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
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; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;
Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEQNSQSDYYEENMGTYDYSOYELICIKEDYREFAKVFLPVLTVFVIGLAGNS 60
DB 1 VCLQDEVTDYIGDNT---TVDYTLFESLCKSKDVRNFKAWFLPIMYSIICFVGLLNG 57

QY 61 MVVAIYAYKKQRTDVTYILNLAVALDILLFTLPFWAVNAVHGVGLKIMCKITSALYT 120
DB 58 LVVLTYYIKRLKTMDDTYLLNLAVALDILLFTLPFWAYSAKSWGVHFCFLIFAIYK 117

QY 121 LNFVSGMQLACISIDRYVAVTKVPS-----QSGVGKPCWIIICFCVWMAILLISIPQLVY 176
DB 118 MSFFGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPPELLYS 177

QY 177 TVNDNA-----RCIPFPRLYGLTSMKALIQMLEICIGFVVPFLMGVCVFITARTLMKMP 231
DB 178 DLORSSSQAMRCSLITEH---VEAFITQVAQWVIGLVPFLANSFCYLVIIIRLLQAR 234

QY 232 NIKISRLKVLTVVIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESTI 291
DB 235 NFERNKAIRKIIAVVVFIVFQLPYNGVLAQTVANFNITSSTCELSKQLNIAYDVYSL 294

QY 292 ALFHSCNLPILYVFMGASFKNVYKAKYG-----SW-----RRQRSVEEFPFD 337
DB 295 ACVRCVNPFLYAFIGVFRNDLFLKFDGLCLSQELQRMSSCRHRRSSMSVE----- 349

QY 338 SEGPTPTSTFS 349
DB 350 ---AETTTTFS 357

RESULT 5
US-09-088-337B-19
; Sequence 19, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
```

```

; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19

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Query Match 36.2%; Score 659; DB 4; Length 358;

Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNQSDYYEENMGTYDYQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60
Db 1 VCLCODEVDDYIGDNT---TVDYTLFESLCSKDVRFKAWFLPTMYSIICFVGLLNG 57
QY 61 MVVAIYAYKKQRTDVTYILNLAVALDLLLFTLPFWAVNAVHGVWLGKIMCKITSALYT 120
Db 58 LVVLYIYFKRLKTDYTLNLAVALDILFLTLFPWYSAKSWVGVHFKLIFAIYK 117
QY 121 LNFVSGMFLACISIDRYVAVTKVPS---QSGVGKPCWIIICFCVWMAAILLSIPQLVY 176
Db 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLLSKLSVGIWILATVLSIPELLYS 177
QY 177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGVFWPFLNGVCFYFARTLMKMP 231
Db 178 DLQSSSQAMRCSLITEH---VEAFITQVQAVMIGFLVPLPMSFCYLVIRTLQAR 234
QY 232 NIKISRLPKLVLTVVIVFIVTQLPYNIKVFCAIDIIYSLITSCNMKRMIDIAIOVTSI 291
Db 235 NFERKAIKVIIVVIVFIVTQLPYNGVVLQAVANFNITSTCSELSQLNIAVDVTSI 294
QY 292 ALFHSLNPILYVFMGAFKYNVMKAKYK-----SW-----RRQRSVEEFPFD 337
Db 295 ACVRCVNPFLYAFYGVKFRNDLFKFLDGLCLSOEQLROWSSCHRIIRSSMSVE----- 349
QY 338 SEGPTPTSTFS 349
Db 350 ---AETTTTFS 357

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RESULT 6

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PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.

```

```

; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-19

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Query Match 36.2%; Score 659; DB 5; Length 358;

Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MALEQNQSDYYEENMGTYDYQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60
Db 1 VCLCODEVDDYIGDNT---TVDYTLFESLCSKDVRFKAWFLPTMYSIICFVGLLNG 57
QY 61 MVVAIYAYKKQRTDVTYILNLAVALDLLLFTLPFWAVNAVHGVWLGKIMCKITSALYT 120
Db 58 LVVLYIYFKRLKTDYTLNLAVALDILFLTLFPWYSAKSWVGVHFKLIFAIYK 117
QY 121 LNFVSGMFLACISIDRYVAVTKVPS---QSGVGKPCWIIICFCVWMAAILLSIPQLVY 176
Db 118 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLLSKLSVGIWILATVLSIPELLYS 177
QY 177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGVFWPFLNGVCFYFARTLMKMP 231
Db 178 DLQSSSQAMRCSLITEH---VEAFITQVQAVMIGFLVPLPMSFCYLVIRTLQAR 234
QY 232 NIKISRLPKLVLTVVIVFIVTQLPYNIKVFCAIDIIYSLITSCNMKRMIDIAIOVTSI 291
Db 235 NFERKAIKVIIVVIVFIVTQLPYNGVVLQAVANFNITSTCSELSQLNIAVDVTSI 294
QY 292 ALFHSLNPILYVFMGAFKYNVMKAKYK-----SW-----RRQRSVEEFPFD 337
Db 295 ACVRCVNPFLYAFYGVKFRNDLFKFLDGLCLSOEQLROWSSCHRIIRSSMSVE----- 349
QY 338 SEGPTPTSTFS 349
Db 350 ---AETTTTFS 357

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RESULT 7
US-08-153-848-15
: Sequence 15, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/153,848
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 378 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 7.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps

QY 1 M A L E O N S T D Y Y E E N M G T Y D S O Y E L I C I K E D Y R E A K V P L P V F L T I V F I G L A G N S 60
DB 21 V C L Q D E V T D Y I G D N P --- T V D Y T L F E S C S K K D V R N F K A W F L P I M Y S I C F V G L L G N G 77
QY 61 M V A I Y A Y K K Q R T K T D V Y I L N L A V A D L L L L F T L P F W A V N A H G V L G K T M C K I T S A L Y T 120
DB 78 L V L V T Y I Y F R L K T W M T D T Y L L N L A V A D I L L L T L P F W A S A A K S W F G V H F C K L I E A I Y K 137
QY 121 L N F V S H G Q F L A C I S I D R Y A V T K V P S --- Q S G V G R K P W I C F C V W M A I L S I P O L V P Y 176
DB 138 M S P F S G M L L L C I S I D R Y A I V Q A V S A H R R A R V L L I S K L S C V G I W I L A T V L S I P E L L Y S 197
QY 177 T V N D N A --- R C I P I P R Y L G T S M K A L I O M L E I C I G F V V P F L I M G V C V F I T A R T L M K M P 231
DB 198 D L Q R S S E Q A M R C S L I T E H --- V E A F T I Q V A Q W I G F L V P L L A M S F C V L V I I R T L L Q A R 254
QY 232 N I K T S R P L K V L L T W I V I F T Q L P Y N I V K F C R A I D I T Y S L I T S C N K S K R M D I A I Q V T E S I 291
DB 255 N F E R N K A I K V I I A V V V F I V Q L P Y N G V L A Q V A N F N I T S T S C E L S K Q L N I A Y D T Y S L 314
QY 292 A L P H S C I N P I L Y I V M G A S F K N Y M K A K Y G - - - - - S W - - - - - R R Q R S V E E F P D 377

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Db 315 ACVRCCNPNFLYAFIGVKFRNDLFKLFKDLGCLISQEQOLROWSSCRHRRSSMSVE----- 367
Qy 338 SEGTEPTSTFS 349
   I :|||
Db 370 ----AETTTFS 377

RESULT 8
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: SchweiKart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; pred. No. 7.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps

Qy 1 MALSQNSTDYDYEEENMGTYDSQVELICIEDVREFAKVLPVFLTIVFVIGLAGNS 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 VCLQCDQEVTDYIDGNT---TVDTYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLG 77
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 MVVAIYAYKKQRTKTDVYIILNLAVADLLLLFTLPFVAVNAVHGVLGKIMKITSALYT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 LVVITYIFRKLKTTDTYLLNLAVADILLLFTLPFVAVNAKSWFGVHFKLIFAIYK 137
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGKPCWITICFVNMAAILLISIPOLVFY 173

```


ATTORNEY/AGENT INFORMATION:
NAME: No. 634857hand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-337B-7

Query Match 36.2%; Score 659; DB 4; Length 410;
Best Local Similarity 38.7%; Pred. No. 7.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEQNSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVFLPVELTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---TVDYTLFESLCKSKKDVRFKAWFLPMYSLICFVGLLNG 109
QY 61 MVVAIYAYKKQRTDVTYILNLAVADLLFLTPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 110 LVVLYIYFKRLKWTDTYLLNLAVADILFLTLFPWAYSAKSWFGVHFCCLIFAIYK 169
QY 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGKPCWICFCVWMAAILLSIPQLVY 176
DB 170 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPRLGTSMKALQMLEICIGFVVPFLMGVCVFITARTLMKMP 231
DB 230 DLQSSSQAMRCSLITEH---VEAFITQVQMVIGFLVPLAMSFCYLVLIIRTLQAR 286
QY 232 NIKISRLKVLVTIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 287 NFERNKAIVIAVAVVVFVQLPYNGVVLQAVANFNITSSSTCCLSKQLNIAVDVYSL 346
QY 292 ALFHSCILNPILYVFMGASFKNYVMKAKYG-----SW-----RRQRQSVVEEPPFD 337
DB 347 ACVRCVNPFLYAFYGVKFRNDLFLKFDGLCLSQEQLQWSSCRHRRSSMSVE----- 401
QY 338 SEGPTPTSTFS 349
DB 402 ----AETTTFS 409

RESULT 15
PCT-US93-11153-7
Sequence 7, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-7
Query Match 36.2%; Score 659; DB 5; Length 410;
Best Local Similarity 38.7%; Pred. No. 7.8e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEQNSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVFLPVELTIVFVIGLAGNS 60
DB 53 VCLQDEVTDDYIGDNT---TVDYTLFESLCKSKKDVRFKAWFLPMYSLICFVGLLNG 109
QY 61 MVVAIYAYKKQRTDVTYILNLAVADLLFLTPFWAVNAVHGVGLGKIMCKITSALYT 120
DB 110 LVVLYIYFKRLKWTDTYLLNLAVADILFLTLFPWAYSAKSWFGVHFCCLIFAIYK 169
QY 121 LNFVSGMQLACISIDRYVAVTKVPS---QSGVGKPCWICFCVWMAAILLSIPQLVY 176
DB 170 MSFFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSCVGIWILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPRLGTSMKALQMLEICIGFVVPFLMGVCVFITARTLMKMP 231
DB 230 DLQSSSQAMRCSLITEH---VEAFITQVQMVIGFLVPLAMSFCYLVLIIRTLQAR 286
QY 232 NIKISRLKVLVTIVFIVTQLPYNIKFCRAIDIIYSLITSCNMKRMIDIAIQVTESI 291
DB 287 NFERNKAIVIAVAVVVFVQLPYNGVVLQAVANFNITSSSTCCLSKQLNIAVDVYSL 346
QY 292 ALFHSCILNPILYVFMGASFKNYVMKAKYG-----SW-----RRQRQSVVEEPPFD 337
DB 347 ACVRCVNPFLYAFYGVKFRNDLFLKFDGLCLSQEQLQWSSCRHRRSSMSVE----- 401
QY 338 SEGPTPTSTFS 349
DB 402 ----AETTTFS 409
Search completed: August 6, 2002, 18:08:28
Job time: 238 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:07:30 ; Search time 13.42 Seconds
(without alignments)
1009.824 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNSTDYEEENMG.....VEEPFDSEGTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	1	CKRE_HUMAN
2	1620	89.1	350	1	CKRE_BOVIN
3	659	36.2	378	1	CKR7_HUMAN
4	650	35.7	378	1	CKR7_MOUSE
5	639	35.1	369	1	CKR9_MOUSE
6	637	35.0	357	1	CKR9_HUMAN
7	605	33.3	367	1	CKR6_MOUSE
8	583	32.1	374	1	CKR6_HUMAN
9	581	31.9	342	1	CCRE_CERAE
10	571	31.4	343	1	CCRE_MACMU
11	569	31.3	342	1	CCRE_MACNE
12	560	30.8	342	1	CCRE_HUMAN
13	537.5	29.5	360	1	CKR4_HUMAN
14	534.5	29.4	360	1	IL8B_HUMAN
15	529.5	29.1	353	1	IL8B_PANTR
16	525	28.9	362	1	CKRA_HUMAN
17	524	28.8	354	1	C3X1_RAT
18	523	28.8	384	1	CKD6_HUMAN
19	522.5	28.7	353	1	IL8B_GORGO
20	522.5	28.7	355	1	C3X1_MOUSE
21	522.5	28.7	360	1	CKR4_MOUSE
22	521.5	28.7	353	1	IL8B_MACMU
23	520.5	28.6	362	1	CKRA_MOUSE
24	512	28.1	356	1	IL8B_CANFA
25	511	28.1	354	1	C3X1_MOUSE
26	511	28.1	358	1	IL8B_RABIT
27	504	27.7	360	1	CKR2_MACMU
28	501.5	27.6	355	1	IL8A_RABIT
29	501.5	27.6	358	1	CKR3_CAVPO
30	500.5	27.5	352	1	CKR4_HUMAN
31	499.5	27.5	353	1	CKR4_BOVIN
32	499.5	27.5	360	1	IL8B_BOVIN
33	498.5	27.4	352	1	CKR4_PAPAN

RESULT 1

ID	CKRB_HUMAN	STANDARD;	PRT;	350 AA.
AC	Q9NPB9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	C-C chemokine receptor type II (C-C CKR-11) (CC-CKR-11) (CCR-11)			
DE	(Chemokine receptor-like 1) (CCL1) (CCX CKR).			
GN	CCR11 OR CCRP2 OR VSHR1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20200450; PubMed=10734104;			
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;			
RT	"CCR11 is a functional receptor for the monocyte chemoattractant			
RT	protein family of chemokines.";			
RL	J. Biol. Chem. 275:9550-9556(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20171478; PubMed=10706668;			
RA	Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,			
RA	Schall T.J.;			
RT	"Cutting edge: identification of a novel chemokine receptor that binds			
RT	dendritic cell- and T cell-active chemokines including ELC, SLC, and			
RT	TECK.";			
RL	J. Immunol. 164:2851-2856(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20231748; PubMed=10767544;			
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamaia V.;			
RT	"Cloning of CCR11, an orphan seven transmembrane receptor related to			
RT	chemokine receptors, expressed abundantly in heart.";			
RL	Gene 246:223-238(2000).			
CC	-1- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYAB/MCP2, SCYA13/MCP4.			
CC	SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER			
CC	EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL			
CC	TISSUES.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
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CC	-----			
DR	EMBL; AF193507; AAF61299.1; -			
DR	EMBL; AF233281; AAF44751.1; -			
DR	EMBL; AF110640; AAF59827.1; -			

062743 cercocobus
P56498 felis silve
P55919 gorilla gor
P56493 cercopithec
062747 cercocobus
Q28474 macaca fasc
P79394 macaca mula
O54814 rattus norv
P35407 rattus norv
P56441 papio hamad
O97880 pygathrix b
P79436 macaca mula

ALIGNMENTS

```

DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 107 POTENTIAL.
FT DOMAIN 109 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 134 POTENTIAL.
FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 POTENTIAL.
FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 290 310 POTENTIAL.
FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60
Db 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60

Qy 61 MVVAIYAYKKQRTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 MVVAIYAYKKQRTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120

Qy 121 LNFVSGMQFLACISIDRYAVATKVPQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 LNFVSGMQFLACISIDRYAVATKVPQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180

Qy 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240
Db 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240

Qy 241 VLLTQVIVFIVTQLPYNIIVAFCAIDIIYSLITSCNKRMDIAIQVTSIALFHSCLNP 300
Db 241 VLLTQVIVFIVTQLPYNIIVAFCAIDIIYSLITSCNKRMDIAIQVTSIALFHSCLNP 300

Qy 301 ILVYFMGASFKNYMKVAKYIGSWRRQRQSVVEFPDSEGTPTSTFSI 350
Db 301 ILVYFMGASFKNYMKVAKYIGSWRRQRQSVVEFPDSEGTPTSTFSI 350

RESULT 2
CKRB_BOVIN STANDARD; PRT; 350 AA.
AC P35350;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-CR-11) (CC-CR-11) (CCR-11)
DE (Possible gustatory receptor type B) (PPRI protein).
GN CCR11.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

```

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RC TISSUE= Tongue;
RX MEDLINE=93326166; PubMed=8392843;
RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;
RT "Identification of novel members of G-protein coupled receptor
RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
CC -!- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.
CC -!- SUBCELLULAR LOCATION: Integrated membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S63848; AAB27547.1; -.
CC PIR; JN0621; JN0621.
CC GCRdb; GCR_0757; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1_1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G_PROTEIN_RECP_FL1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_FL2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 66 1 (POTENTIAL).
FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 114 135 3 (POTENTIAL).
FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 222 5 (POTENTIAL).
FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 306 7 (POTENTIAL).
FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 112 184 BY SIMILARITY.
SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.8e-92;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALEQNSTDYIYENENMGTYDSQVELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60
Db 1 MAVEYQSDYDYIYENENMGTYDSQVELICIKEDVREFAKVFLPVLFTIVFVIGLAGNS 60

Qy 61 MVVAIYAYKKQRTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 TVVAIYAYKKRRTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120

Qy 121 LNFVSGMQFLACISIDRYAVATKVPQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 VNFVSGMQFLACISIDRYAVATKVPQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180

Qy 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240
Db 181 KARCVPFIFHYLGTSKALIQMLEICIGFVVPFLMGVCYFIFARTLMKPNKISRPLK 240

```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/CBA; TISSUE=Thymus; PubMed=7851893;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Report C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse Ebt1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; L31580; AAA74232.1; -;
 DR MGD; MGI:103011; Cnkb77.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
 FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 60 86 1 (POTENTIAL).
 FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 116 2 (POTENTIAL).
 FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 131 152 3 (POTENTIAL).
 FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 4 (POTENTIAL).
 FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 220 247 5 (POTENTIAL).
 FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 264 289 6 (POTENTIAL).
 FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 314 331 7 (POTENTIAL).
 FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 129 210 BY SIMILARITY.
 SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AA54 CRC64;

Query Match 35.7%; Score 650; DB 1; Length 378;
 Best Local Similarity 38.3%; Pred. No. 2.6e-33;
 Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNOSTDYEEENMGTYDSQYELICKEDEVFAKFLPVELTIVFVIGLAGNSMVA 64
 DB 25 ODEVTDDYIGENT---TVDYTLVESVCFKDVNRKAWFLPLMVSIVCFVGLLGNGLVIL 81
 QY 65 IYAYKKORTKTDVYILNLAVALLLLTLPFVAVNAVHGVGLKIMKITSALYTLNFV 124
 DB 82 TTYIFRKLTKMTDTLLNLAVALLLLTLPFWAYSEAKSWIFGVLCKGFGYKLSFF 141
 QY 125 SGMOFLACISIDRYAVTKVPSQS-----VGKPCWICFCVYMAALLSIPOLVYPT 177
 DB 142 SGMLLLLCISIDRYVAIVQVSRHRRARVLLISK---LSCVGIWMLALFSLPELYSG 198
 QY 178 VNDNA-----RCIFPFLYGLTSKAL--IQMLEICIGFVVPFLMGVCYFIFARTLMKM 230
 DB 199 LQKNSGDTLRC-----SLVSAQVEALITIQVAQMFGLVPLMAMSFVCLIIIRTLQA 253

QY 231 PNKISRLPKVLLTWVIVTQLPYINIVKFCRAIDIIYSLITSCNMSKRMDAIOVTES 290
 DB 254 RNFRNKAIKVIIVAVVVFIVFQLPYNGVYLAQTVANFNITNSCETSOLNAYDVTYS 313
 QY 291 IALFHSCLNPLXYFMGASFKNYVMKAKYKGSRROR-----QSVVEFPDSECPTE 343
 DB 314 LASVRCVNPFLYAFIGVKFRSDFLKLFDGLCSQERLHNSCRHVRNASVSMB--AE 371
 QY 344 PTSTFS 349
 DB 372 TTTTFS 377

RESULT 5
 CKR9_MOUSE
 ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WU7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
 DE (Chemokine C-C receptor 10).
 GN CKR9 OR CMKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: Identification of the orphan chemokine receptor GPR-9-6
 RL as CCR9, the receptor for the chemokine TECK.";
 RL J. Immunol. 162:5671-5675(1999).
 CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AJ132336; CAB43480.1; -;
 DR MGD; MGI:1341902; Cnkb10.
 DR InterPro; IPR004069; Chemokine9_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01531; CHEMOKINER9.
 DR PRINTS; PR00237; GPCRRHODOPS.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 76 1 (POTENTIAL).
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 2 (POTENTIAL).
 FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181 4 (POTENTIAL).
 FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 238 5 (POTENTIAL).
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).


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FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 164 4 (POTENTIAL).
FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 215 5 (POTENTIAL).
FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 180 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 60BFE39C6E5919E CRC64;

Query Match 31.98; Score 581; DB 1; Length 342;
Best Local Similarity 34.28; Pred. No. 3.9e-29;
Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

Qy 12 YVEENMGTYDYSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNSMVVAIYAYKK 71
    :||:| | | | | :| :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 6 HYEDNGFNSDSQEE---HQDFLOFSKVFLPCMYLVFVCGLVGNSLVLSIFYHK 61

Qy 72 QRTKTDVILNLAVADLLLTLPFWAVNAVHGVGLKIMCKITSAIYTLNFSVGMQFLA 131
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 62 LQSLTDVFLNPLADLVFVCTLPFWAYAGIHEWIFGQVMCKTLIGIYVTFNYTSMILT 121

Qy 132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVMAAILLSIPOLVFYTV--NDNARCI 185
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 122 CITVDRFVIVVVKATKAYNOQAKMTGWKVICLLIWSLVSLPQIYIGNVFNLDKLC- 180

Qy 186 PIFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTKMPNLIKISRLKVLTV 245
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 181 ----GYHDEEISTVVLATQMTLGFPLLAMIVCVSVIITKLLHAGGFKHRSKLIIFLV 236

Qy 246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNPILYVF 305
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 237 MAVLFTLTQTPFNLVKLIIRSTHWEIYAMTSFHYT-----IIVTEAIAYLRACLNPVLYAF 290

Qy 306 MGASFKNVVMKVAKYG-----SWRRQRQSVVEEFPDFSEGTPTSTFSI 350
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 291 VSLAKFRKFWKLVKDIGCLPYLVGVSHQWKSSEDNSK--TFSASHNVATSMFQL 342

RESULT 10
CCR6_MACMU STANDARD; PRT; 343 AA.
ID Q9XT45;
AC Q9XT45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo) (G protein-coupled receptor STRL33).
GN CXCR6 OR BONZO OR STRL33.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF124380; AAD31419.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW EXTRACELLULAR (POTENTIAL).
DB DOMAIN 1 33
FT TRANSMEM 34 60 1 (POTENTIAL).
FT DOMAIN 61 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 3 (POTENTIAL).
FT DOMAIN 127 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 165 4 (POTENTIAL).
FT DOMAIN 166 188 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 189 216 5 (POTENTIAL).
FT DOMAIN 217 232 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 233 260 6 (POTENTIAL).
FT DOMAIN 261 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 294 7 (POTENTIAL).
FT DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC... ) (POTENTIAL).
FT DISULFID 103 181 BY SIMILARITY.
SQ SEQUENCE 343 AA; 48DB2544949EB83F CRC64;

Query Match 31.44; Score 571; DB 1; Length 343;
Best Local Similarity 33.44; Pred. No. 1.6e-28;
Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

Qy 10 DYYVEENMGTYDYSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNSMVVAIYAY 69
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 5 DHYEDDGFNSDSQEE---HQDFLOFSKVFLPCMYLVFVCGLVGNSLVLSIFY 60

Qy 70 KQRTKTDVILNLAVADLLLTLPFWAVNAVHGVGLKIMCKITSAIYTLNFSVGMQF 129
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 61 HKLQSLTDVFLNPLADLVFVCTLPFWAYAGIHEWIFGQVMCKTLIGIYVTFNYTSMIL 120

Qy 130 LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVMAAILLSIPOLVFYTV--NDNAR 183
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 121 LTCITVDRFVIVVVKATKAYNOQAKMTGWKVICLLIWSLVSLPQIYIGNVFNLDKLI 180

Qy 184 CIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARLTKMPNLIKISRLKVL 243
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 181 C-----GYHDEEISTVVLATQMTLGFPLLAMIVCVSVIITKLLHAGGFKHRSKLIIF 235

Qy 244 TVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNPILY 303
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 236 LVMAVFLTLTQTPFNLVKLIIRSTHWEIYAMTSFHYT-----IIVTEAIAYLRACLNPVLY 289

Qy 304 VFMGASFKNVVMKVAKYG-----SWRRQRQSVVEEFPDFSEGTPTSTFSI 350
    :||:| | | | | :||:| | | | | :||:| | | | | :||:| | | | | :||:|
Db 290 AFVSLKFRKFWKLVKDIGCLPYLVGVSHQWKSSEDNSK--TFSASHNVATSMFQL 343

RESULT 11
CCR6_MACNE STANDARD; PRT; 342 AA.
ID O19024;
AC O19024;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo).
GN CXCR6 OR BONZO.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


DR	EMBL; AB023890; BAA86967.1; -	DE	High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
DR	EMBL; AB023891; BAA86968.1; -	DE	receptor) (IL-8 receptor type 2) (CDw128b).
DR	EMBL; AB023892; BAA86969.1; -	GN	IL8RB OR CXCR2.
DR	GCRDb; GCR_21115; -	OS	Homo sapiens (Human).
DR	MIM; 604836; -	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	InterPro; IPR000276; GPCR_Rhodospn.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
DR	Pfam; PF00001; 7tm_1; 1.	OX	NCBI_TaxID=9606;
DR	PRINTS; PR00237; GPCRRHODOPS.	RN	[1]
DR	PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.	RP	SEQUENCE FROM N.A.
DR	PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.	RX	MEDLINE-91368200; PubMed-1891716;
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	RA	Murphy P.M., Tiffany H.L.;
KW	Phosphorylation; Polymorphism.	RT	"Cloning of complementary DNA encoding a functional human
FT	DOMAIN 1 39	RT	interleukin-8 receptor.";
FT	TRANSMEM 40 67	RL	Science 253:1280-1283(1991).
FT	DOMAIN 68 77	RN	[2]
FT	TRANSMEM 78 98	RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
FT	DOMAIN 99 111	RX	MEDLINE-93205012; PubMed-8384312;
FT	TRANSMEM 112 133	RA	Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
FT	DOMAIN 134 150	RA	Beckmann M.P.;
FT	TRANSMEM 151 175	RT	"Molecular characterization of receptors for human interleukin-8,
FT	DOMAIN 176 206	RT	GRO/melanoma growth-stimulatory activity and neutrophil activating
FT	TRANSMEM 207 226	RT	peptide-2.";
FT	DOMAIN 227 242	RL	Mol. Immunol. 30:359-367(1993).
FT	TRANSMEM 243 267	RN	[3]
FT	DOMAIN 268 284	RP	SEQUENCE FROM N.A.
FT	TRANSMEM 285 308	RX	MEDLINE-94209273; PubMed-7512557;
FT	DOMAIN 309 360	RA	Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
FT	CARBOHYD 183 183	RT	"Structure, genomic organization, and expression of the human
FT	CARBOHYD 194 194	RT	interleukin-8 receptor B gene.";
FT	DISULFID 110 187	RL	J. Biol. Chem. 269:11065-11072(1994).
FT	VARIANT 130 130	RN	[4]
FT	VARIANT 178 178	RP	SEQUENCE FROM N.A.
FT	VARIANT 178 178	RC	TISSUE=Placenta;
FT	SEQUENCE 360 AA; 41402 MW; 51EBE12AD1FAFABP CRC64;	RX	MEDLINE-95014476; PubMed-7929358;
FT		RA	Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
FT		RT	"Comparison of the genomic organization and promoter function for
FT		RT	human interleukin-8 receptors A and B.";
FT		RL	J. Biol. Chem. 269:26381-26389(1994).
FT		RN	[5]
FT		RP	CHARACTERIZATION.
FT		RX	MEDLINE-92355587; PubMed-1379593;
FT		RA	Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
FT		RT	"Characterization of two high affinity human interleukin-8
FT		RT	receptors.";
FT		RL	J. Biol. Chem. 267:16283-16287(1992).
FT		CC	-1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
FT		CC	NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
FT		CC	CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
FT		CC	G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
FT		CC	MESSANGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
FT		CC	AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
FT		CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
FT		CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FT		CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CDw128b entry;
FT		CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".
FT		CC	-----
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FT		CC	or send an email to license@isb-sib.ch).
FT		CC	-----
FT		CC	EMBL; M73969; AAA83148.1; -
FT		DR	EMBL; M94582; AAA36108.1; -
FT		DR	EMBL; M99412; AAC14460.1; -
FT		DR	EMBL; L19593; AAB59437.1; -
FT		DR	EMBL; U11869; AAB60656.1; -
FT		DR	PIR; A39446; A39446.
FT		DR	PIR; A53611; A53611.
FT		DR	HSSP; P34996; IDDD.
FT		DR	GCRDb; GCR_0077; -
FT		DR	
QY	10 DYYEENENMGYDYSQYELICKEDVREFAKVLFPVLTIVFVIGLAGNSWVAIYAY 69	Query Match	29.5%; Score 537.5; DB 1; Length 360;
DB	8 DTTLDEISYNNLYSIESIPKPKTEGIRKAFGELPPLYSLVFVGLGNSVVVLVLFY 67	Best Local Similarity	35.8%; Pred. No. 1.8e-26;
QY	70 KKQRTDYYILNLAVALDLLLTLPFAVNAVHVGWLGKIMCKITFSALYTLNFVSGMOF 129	Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;	
DB	68 KRLRSTWYLLNLAISDLLFVFSLPFWGYAQQWVFGLGCKMISWYLVGYSGIFF 127		
QY	130 LACISIDRYVAVTKV-----PSQSGVGKPCWICFCVYMAAILLSIFQLVF---YTVN 179		
DB	128 VMLMSIDRYLAIVHAFVLSRARTLTGV-----ITSLATWSAVAFASLPGLFSTCYTER 182		
QY	180 DNARCIPFPRLVLTGSKALQIOMLEI-CIGFVVPFLMGVCYFITAATLMKPNKNIISRP 238		
DB	183 NHTYCTKYS--LNSYTWKVLSSLEINILGVLPIGLMFLCYSMIIRTLQHCNKNEKKA 240		
QY	239 LKVLTVWIVFVITQLPYNVFRCAIDIIYSLTSCNNSKRMIDIAIQVTESTALPHSCL 298		
DB	241 VKMIFAVVVLFGFTWPTYNIVLFLETL-VELEVLOQCTERYLDYAIQATETLAFVHCCL 299		
QY	299 NPILYVFMGASPKNYVMKAV 319		
DB	300 NPILYVFMGASPKNYVMKAV 319		
RESULT 14			
IL8B_HUMAN			
ID	IL8B_HUMAN	STANDARD;	PRT; 360 AA.
AC	P25025;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		

Qy	118	LYTLNFVSGHQFLACISIDRYAV--TKVPSSGVGKFCWICFCVMAAILLSTPQLV	174
Db	122	LKEVNFSGILLACISVDRLAIVHATRTQKRY--LVKFCILSINGLSLLALLPVLL	179
Qy	175	F----YVNVNDARCIPFPRLG--TSMKALQMLEICIGFVWPPLINGVCYETARTL	227
Db	180	FRTVYSSNVSPACY----EDMGNNTANWRMLRMLPQSGFGFVLPULLMLFCYGFTRL	235
Qy	228	MKMPNIKISRLPLVLLTVFVTQLPYNIVKFCRAIDIIYSLITSCHNSKRMIDIAQV	287
Db	236	FKAHMGQKHRAMRIFAVVLFIELCWLPTYNLVLLADTLMTQVIQETCERRNHINRALDA	295
Qy	288	TESTALPHSCNLPLYVFMGASPKNYVMKVKYGSNRQRORQSVSEFFPDS	338
Db	296	TEIGLIHSCNLPLYAFIQGKPRHGLLTLIAHGT-----LTSKDSLPKDS	341

Search completed: August 6, 2002, 18:09:48
Job time: 138 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 17:57:40 ; Search time 32.78 Seconds
(without alignments)
1185.962 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNQSTDYIYENEMNG.....VEEFPDSEGTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	20	AA1980
2	1819	100.0	350	20	AA1981
3	1819	100.0	350	20	AA1982
4	1819	100.0	350	20	AA1983
5	1819	100.0	350	20	AA1984
6	1819	100.0	350	20	AA1985
7	1819	100.0	350	20	AA1986
8	1819	100.0	350	20	AA1987
9	1814	99.7	349	20	AA1988
10	1814	99.7	350	20	AA1989
11	1810	99.5	350	21	AA1990

12	1810	99.5	350	21	AA1980
13	1808	99.4	350	21	AA1981
14	1728	95.0	333	20	AA1982
15	1620	89.1	350	22	AA1983
16	1591	87.5	350	20	AA1984
17	1275	70.1	246	20	AA1985
18	1257	69.1	242	22	AA1986
19	1212	66.6	263	20	AA1987
20	862	47.4	164	22	AA1988
21	862	47.4	164	22	AA1989
22	824	45.3	159	21	AA1990
23	761	41.8	175	22	AA1991
24	761	41.8	175	22	AA1992
25	761	41.8	175	22	AA1993
26	761	41.8	175	22	AA1994
27	761	41.8	175	22	AA1995
28	761	41.8	175	22	AA1996
29	659	36.2	358	15	AA1997
30	659	36.2	358	21	AA1998
31	659	36.2	378	19	AA1999
32	659	36.2	378	21	AA2000
33	659	36.2	378	22	AA2001
34	659	36.2	378	22	AA2002
35	659	36.2	410	15	AA2003
36	659	36.2	410	19	AA2004
37	659	36.2	410	21	AA2005
38	659	36.2	569	22	AA2006
39	656	36.1	378	15	AA2007
40	655	36.0	378	21	AA2008
41	653	35.9	378	21	AA2009
42	650	35.7	378	21	AA2010
43	643	35.3	369	22	AA2011
44	643	35.3	378	15	AA2012
45	643	35.3	378	19	AA2013

ALIGNMENTS

RESULT 1

AA1980
ID AA1980 standard; Protein; 350 AA.

AA1981

05-JUN-2000 (first entry)

Human BGCR protein.

BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;
cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
anti-allergic; antiviral.

Homo sapiens.

WO9952945-A2.

21-OCT-1999.

16-APR-1999; 99WO-US08395.

16-APR-1998; 98US-0061753.

16-APR-1999; 99US-0061753.

(MILL-) MILLENIUM PHARM INC.

Gonzalo JA, Gutierrez-Ramos JC;

WPI: 1999-620375/53.

N-PSDB; AA290528.

New nucleic acid encoding human BGCR receptor, used e.g. for
modulating inflammation and tumor growth

```
XX PS Claim 8; Fig 2A-B; 123pp; English.
XX CC The invention relates to a human BGCKr protein, a G-protein coupled
XX CC receptor. The BGCKr protein can be expressed by standard recombinant
XX CC methodology. BGCKr are receptor proteins possibly involved in modulation
XX CC of proinflammatory or stimulatory functions of chemokines; cell
XX CC proliferation, migration, adhesion and targeting, and exocytosis. The
XX CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
XX CC and modulators are potentially useful for modulating inflammation;
XX CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
XX CC tumour growth; allergic reactions and entry of human immune deficiency
XX CC virus into cells, for therapeutic or prophylactic purposes. They are also
XX CC used for diagnosis and in drug-screening assays. The present sequence
XX CC represents the full-length human BGCKr protein.
XX SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSTDYEEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 1 maleqngstdyeeenemngtydysqyellicikedvrefakvflpvlftivfvglagns 60
QY 61 MVVAIYAYKKORTDVIYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 mvvaiyaykkortdviylnlavaddlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVGKPCWICFCVWMAAILLSIPOLVFYTVND 180
DB 121 lnfvsqmqflacisidryavatkvpqsogvgkpcwlicfcvwmaaillspqlvfytvnd 180
QY 181 NARCIPFPRLYGTSMKALIQMLEICIGFVVPFLMGVCFYFARTLMKMPNIIKSRLPK 240
DB 181 narcipfprrlygtsmkalilqmlaicigfvpvflmgvcyfartlmkmpniiksrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYVKFCRAIDIIYSLITSCNMKRMIDIAIOVTESIALFHSCNLP 300
DB 241 vlltvvfvivtqlpyniyvkfcradiliiyslitscnmskrmdiaiovtesialfhscnlp 300
QY 301 ILVFMGASFKNYVMKVAKKYGSRRQRQSVVEEFPDSEGPTEPTSTFSI 350
DB 301 ilvfmgasfknymkvakkygsrrqrqsvveefpdsgeptstfsi 350

RESULT 2
AA17435
ID AA17435 standard; Protein; 350 AA.
XX AC AA17435;
XX DT 29-JUL-1999 (first entry)
XX DE Human signal peptide-containing protein SP-16.
XX KW Human; signal peptide-containing protein; SP; cell proliferation;
XX KW cancer; neuronal disorder; immune response; detection.
XX OS Homo sapiens.
XX PN WO9924463-A2.
XX PD 20-MAY-1999.
XX PF 04-NOV-1998; 98WO-US23578.
XX PR 07-NOV-1997; 97US-0966316.
XX PA (INCY-) INCYTE PHARM INC.
XX OS Homo sapiens.

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
XX WPI; 1999-337694/28.
XX DR N-PSDB; AAX61288.
XX CC cDNA clones encoding signal peptide-containing proteins
XX PS Claim 1; Fig 1; 83pp; English.
XX CC The present sequence represents a human signal peptide-containing
XX CC protein (SP), designated SP-16. SP proteins can be used to stimulate
XX CC cell proliferation or to treat or prevent cancer. SP antagonists are
XX CC also used to treat or prevent cancer, and also for treating or
XX CC preventing neuronal disorders or immune responses. Polynucleotide
XX CC sequences complementary to the SP-encoding polynucleotides are useful
XX CC for the detection of SP-encoding nucleic acid molecules in biological
XX CC samples.
XX SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSTDYEEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
DB 1 maleqngstdyeeenemngtydysqyellicikedvrefakvflpvlftivfvglagns 60
QY 61 MVVAIYAYKKORTDVIYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
DB 61 mvvaiyaykkortdviylnlavaddlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPQSOGVGKPCWICFCVWMAAILLSIPOLVFYTVND 180
DB 121 lnfvsqmqflacisidryavatkvpqsogvgkpcwlicfcvwmaaillspqlvfytvnd 180
QY 181 NARCIPFPRLYGTSMKALIQMLEICIGFVVPFLMGVCFYFARTLMKMPNIIKSRLPK 240
DB 181 narcipfprrlygtsmkalilqmlaicigfvpvflmgvcyfartlmkmpniiksrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYVKFCRAIDIIYSLITSCNMKRMIDIAIOVTESIALFHSCNLP 300
DB 241 vlltvvfvivtqlpyniyvkfcradiliiyslitscnmskrmdiaiovtesialfhscnlp 300
QY 301 ILVFMGASFKNYVMKVAKKYGSRRQRQSVVEEFPDSEGPTEPTSTFSI 350
DB 301 ilvfmgasfknymkvakkygsrrqrqsvveefpdsgeptstfsi 350

RESULT 3
AAW93169
ID AAW93169 standard; Protein; 350 AA.
XX AC AAW93169;
XX DT 24-MAY-1999 (first entry)
XX DE Human HETA041 protein.
XX KW HETA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
XX KW treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2;
XX KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
XX KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
XX KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
XX KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
XX KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
XX KW anxiety; manic depression; delirium; dementia; severe mental retardation;
XX KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
XX KW linkage analysis; gene mapping; human.
XX OS Homo sapiens.
```

PN EP899332-A2.
XX 03-MAR-1999.
XX 17-FEB-1998; 98EP-0301170.
XX 27-OCT-1997; 97US-0962922.
PR 15-AUG-1997; 97US-0055895.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Ellis CE;
XX WPI; 1999-144803/13.
DR N-PSDB; AAX22557.
XX
XX New G-coupled receptor (HFA041) polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease
XX
XX Claim 1; Page 22-23; 27pp; English.
XX
XX This sequence represents a G-coupled receptor, HFA041 which is useful
CC for diagnosing susceptibility to diseases by detecting mutations in the
CC HFA041 gene, and can diagnose diseases associated with HFA041 protein
CC imbalance by determining HFA041 polypeptide expression levels. Agonists
CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) HFA041 activity, in addition to direct
CC administration of antisense sequences to prevent expression, or HFA041
CC polynucleotides to treat conditions associated with a lack of HFA041
CC protein. Gene therapy may also be used to affect endogenous HFA041
CC polypeptide expression. HFA041 antibodies are useful for inducing an
CC immune response to immunise and prevent disease, and for isolating
CC HFA041 clones or purifying the polypeptides by affinity chromatography.
CC HFA041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergies; benign prostatic hypertrophy; and psychoticic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC HFA041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.
XX
XX Sequence 350 AA;
SQ

Query Match 100.0%; Score 1819; DB 20; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALEONQSTDYIYENENMGTYDSQYELICKEDVREFAKVPFLTVFVIGLAGNS 60
Db 1 maleqnqstdyvyeenmgtydsqyelickedvrefakvlpvftivfvlagns 60

Qy 61 MVVATYAYKKQRTDYYIINLAVADLLLTLPFAVNAVHGVGLCKIMCKITSALYT 120
Db 61 mvvalyaykkqrktddyvlinlavadllltlfpfavnvavhgvglckimckitsalyt 120

Qy 121 LNFVSGMFLACISIDRYVAVTKVPSQSGVKGPCWIIICFVWMAAILLSIPQLVFYTVND 180
Db 121 lnfvsqgmflacisidryvavtkvpsqsgvkpcwliicfcvmaailisipqlvfytvnd 180

Qy 181 NARCIPFPRIYLGTSKALIQMLETCIGFVFPFLTMGVCYFITATLKMKNPKISRLPK 240
Db 181 narcipifprijlgtskalmleicigfvyvfpfltmgvcyfitatlmkmpnikisrplk 240

Qy 241 VLLTVVIVFIVTOLPVNIVKFCRAIDIIYSLITSNCMSKRMWDIAIQVTFESIALFHSCLNP 300
Db 241 vlltvvfvitvqpvynivkvkrcraidiiylsitsncmskrmdiaiqvtesialfhscinp 300

Qy 301 ILYVFMGASFKNYVMKVAKKYGSWRQRQSVVEFPFDSGPTPTSTFSI 350
Db 301 ilyvfmgsfknymkvakkygswrrqrqsvvefpfdsegptptstfsi 350

RESULT 4
AAY94325
ID AAY94325 standard; Protein; 350 AA.
XX
AC AAY94325;
XX
DT 11-AUG-2000 (first entry)
XX
DE Human seven transmembrane receptor VSHK-1.
XX
KW Human; seven transmembrane receptor; VSHK-1; signal transduction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6..8
FT Modified-site /note= "potential N-glycosylation site"
FT Modified-site 19..21
FT Domain /note= "potential N-glycosylation site"
FT Domain 42..66
FT Domain /label= Transmembrane_domain
FT Domain 79..100
FT Domain /label= Transmembrane_domain
FT Domain 114..135
FT Domain /label= Transmembrane_domain
FT Domain 156..175
FT Domain /label= Transmembrane_domain
FT Domain 199..221
FT Domain /label= Transmembrane_domain
FT Domain 241..262
FT Modified-site 276..278
FT Domain /note= "potential N-glycosylation site"
FT Domain 287..308
FT /label= Transmembrane_domain
XX WO200026369-A1.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25848.
XX
XX 04-NOV-1998; 98US-0107112.
XX 06-JAN-1999; 99US-0114856.
XX
XX (CHIR) CHIRON CORP.
XX
XX Khoja H, Shymala V;
XX WPI; 2000-365618/31.
XX N-PSDB; AAY94325.
XX
XX Novel polypeptide comprising a new seven-transmembrane receptor protein
XX and its encoding polynucleotide, useful for the analysis of VSHK-1 -
PS Claim 3; Fig 1; 79pp; English.
XX
XX The present sequence is VSHK-1, a new seven transmembrane
XX receptor which contains seven membrane-spanning helical domains
XX that are linked by three intracellular and three extracellular loops. The
XX gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart
XX tissue, where VSHK-1 is predominantly found, three RNA species were
XX identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide
XX encoding the present sequence corresponds to the 2.0kb form. The 1.3kb
XX form may result from the use of an alternative polyadenylation site while
XX transcription of a 3.0kb intron at nucleotide 74 could account for the
XX 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes

CC to detect and measure VSHK-1 mRNA. They may also be used to identify
 CC substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding
 CC sequence can be integrated into an expression vector for production of
 CC VSHK-1 receptor polypeptides in host cells. The polypeptides can be used
 CC to identify agents which modulate VSHK-1 receptor signal transduction
 CC activity.

XX Sequence 350 AA;
 SQ
 Query Match 100.0%; Score 1819; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALEQNSQTDYYEENEMNGTYDSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNS 60
 DB 1 maleqnsqtdyyeenemngtydsqyelickedvrefakvflpvlctivfiviglagns 60
 QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
 DB 61 mvvaiyaykkqrtktdivyilnlavadlllftlpfwavnavhgvlgkimckitsalyt 120
 QY 121 LNFVSGMFLACISIDRYAVTVKPSQSGVGKPCWIIICFCVWMAAILLSIPOLVFTYVND 180
 DB 121 lnfvsgmflacisidryavtkvpsqsgvgkpcwiiicfcvwmiaillslpqlvfytynd 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
 DB 181 narcipiprylgtsmkalligleicigfvpflmgvcyfitartlmkmpnikisrplk 240
 QY 241 VLLTVVIVFTQLPYNIYKFCRAIDIYSLITSCNMSKRMIDIAIQVTESTIALFHSCLNP 300
 DB 241 vlltvvivftqlpynivkfcraidiyslitscnmskrmdiaiqvtestialfhscinp 300
 QY 301 ILVFMGASFKNYVMKAKYKGSWRQRQSVVEEPFDSGTEPTSTFSI 350
 DB 301 ilvfmgasfknymkvakkygswrrqrqsvveefpdsgeptstfsi 350

RESULT 5

AG80119
 ID AAG80119 standard; Protein; 350 AA.
 XX
 AC AAG80119;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CRI1 protein.
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN WO200172830-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-EP03708.
 XX
 PR 31-MAR-2000; 2000DE-1016013.
 XX
 PA (IPFP-) IPF PHARM GMBH.
 PA (FORS/) FORSSMANN U.
 XX
 PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
 XX
 DR WPI; 2001-626256/72.
 XX
 XX Diagnostic agent containing two or more receptor-specific ligands,
 PT

PT useful for detecting tumors, inflammation etc., also therapeutic use of
 PT ligand inhibitors -
 XX
 PS Disclosure; Page 11; 26pp; German.

XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention.

XX Sequence 350 AA;
 SQ

Query Match 100.0%; Score 1819; DB 22; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSQTDYYEENEMNGTYDSQYELICIKEDVREFAKVFLPVLTVIVFVIGLAGNS 60
 DB 1 maleqnsqtdyyeenemngtydsqyelickedvrefakvflpvlctivfiviglagns 60
 QY 61 MVVAIYAYKKQRTKTDVYILNLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
 DB 61 mvvaiyaykkqrtktdivyilnlavadlllftlpfwavnavhgvlgkimckitsalyt 120
 QY 121 LNFVSGMFLACISIDRYAVTVKPSQSGVGKPCWIIICFCVWMAAILLSIPOLVFTYVND 180
 DB 121 lnfvsgmflacisidryavtkvpsqsgvgkpcwiiicfcvwmiaillslpqlvfytynd 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLK 240
 DB 181 narcipiprylgtsmkalligleicigfvpflmgvcyfitartlmkmpnikisrplk 240
 QY 241 VLLTVVIVFTQLPYNIYKFCRAIDIYSLITSCNMSKRMIDIAIQVTESTIALFHSCLNP 300
 DB 241 vlltvvivftqlpynivkfcraidiyslitscnmskrmdiaiqvtestialfhscinp 300
 QY 301 ILVFMGASFKNYVMKAKYKGSWRQRQSVVEEPFDSGTEPTSTFSI 350
 DB 301 ilvfmgasfknymkvakkygswrrqrqsvveefpdsgeptstfsi 350

RESULT 6

AAU08994
 ID AAU08994 standard; Protein; 350 AA.
 XX
 AC AAU08994;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human G protein-coupled receptor, GPCR, 2398.
 XX
 KW Human; GPCR; G protein-coupled receptor; 2398; cardiant;
 KW antiatherosclerotic; analgesic; cytostatic; antianginal;
 KW cardiovascular disorder; angiogenesis-related disorder;
 KW neural disorder; pain response disorder; inflammatory disorder;
 KW atherosclerosis; angina pectoris; myocardial infarction;
 KW ischaemic heart disease; sudden cardiac death; obesity;
 KW hypertensive heart disease; diabetes; prostate cancer-related pain.
 XX
 OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Region 125..141
FT /label= G_protein_receptor_signature
XX WO200164882-A2.
XX 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US06543.
XX 29-FEB-2000; 2000US-186059P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Galvin KM, Sillos-Santiago I;
XX WPI: 2001-589866/66.
XX N-PSDB; AAS14572.
XX Novel G protein coupled receptors and nucleic acids encoding them, for
PT identifying agents for the treatment of cardiac disorders -
XX Claim 9; Fig 9; 209pp; English.
XX The invention relates to novel human G protein-coupled receptors (GPCR)
CC named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and
CC nucleic acids encoding them are useful for identifying agents for the
CC treatment of cardiovascular disorders, angiogenesis-related disorders,
CC neural disorders, pain response disorders and inflammatory disorders
CC e.g. atherosclerosis, angina pectoris and myocardial infarction,
CC ischaemic heart disease, sudden cardiac death, hypertensive heart
CC disease, diabetes, prostate cancer-related pain, diabetes and obesity.
CC The present sequence represents GPCR 2398.
XX
SQ Sequence 350 AA;
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEQNQSTDYEEENMGTYDYSQYELICIKEDVREFAKVPFLPVLTVFVIGLAGNS 60
Db 1 maleqnqstdyeeenmgtydysqyelickedvrefakvflpvlftivfvlagns 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 mvvaiyaykkrtkttdvylnlavadvlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGRPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsqmqflacisidryvavtkvpqsgvgkpcwliicfcvwmaaillslpqlvftvnd 180
QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
Db 181 narcipfpryigtcmkallqmeicigfvpflmgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVQLPNVIVKFCRAIDIIYSLITSCNMKRMEDIAIOVTESIALFHSCLNP 300
Db 241 vllttvvivfivqlpnyivkvfcradiliiyslitscnmskrmdiaioqvtesialfhsclnp 300
QY 301 ILIYFMGASFKNYMKVAKYGSRRQRQSVVEFPDSEGPTEPTSTFSI 350
Db 301 iliymgasfknymkvakyswrrqrqsvvefpdsegptstfsi 350
RESULT 7
AAG67237
ID AAG67237 standard; Protein; 350 AA.
XX
AC AAG67237;
XX

DT 13-NOV-2001 (first entry)
XX Amino acid sequence of human chemokine receptor CCR11.
XX
KW Human; chemokine receptor; CCR11; G protein coupled receptor;
KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; atherosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction;migraine; preterm labour;
KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosis;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
XX
OS Homo sapiens.
XX WO200166598-A2.
XX 13-SEP-2001.
XX 05-MAR-2001; 2001WO-US07073.
XX 03-MAR-2000; 2000US-0186928.
XX 03-MAR-2000; 2000US-0187231.
XX (ICOS-) ICOS CORP.
XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
XX WPI: 2001-541918/60.
XX N-PSDB; AAH77711.
XX An isolated polynucleotide encoding the chemokine receptor CCR11,
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine -
XX
PS Claim 13; Page 96-97; 110pp; English.
XX
CC The present sequence represents the human chemokine receptor CCR11.
CC CCR11 is a member of the G protein coupled receptor family. A CCR11
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
CC expression or biological activity, is useful for treating many
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
CC bowel disease, and asthma. They are also useful for treating
CC angioneu, atherosclerosis vascular association diseases which may
CC include but are not limited to hypertension, angina pectoris, cardiac
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
CC pulmonary vascular disease.
XX
SQ Sequence 350 AA;
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEQNQSTDYEEENMGTYDYSQYELICIKEDVREFAKVPFLTVFVIGLAGNS 60
Db 1 maleqnqstdyeeenmgtydysqyelickedvrefakvflpvlftivfvlagns 60
QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120
Db 61 mvvaiyaykkrtkttdvylnlavadvlllftlpfwavnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGRPCWIIICFCVWMAAILLSIPQLVFTVND 180
Db 121 lnfvsqmqflacisidryvavtkvpqsgvgkpcwliicfcvwmaaillslpqlvftvnd 180
QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
XX

Db 181 narcipifprylgtemkallgmleicigfvvpflimgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMKSRMDIAIQVTSIALFHSLNP 300
Db 241 vlltvvifvltqplnykvkfcraidiyslitscnmskrmdiaiqvtsialfhslnp 300
QY 301 ILYVFMGASFKNYVMKVAKYGSRRQRQSVVEFPDSEGPTPTSTFSI 350
Db 301 illyvmgaskfnyvmkvakkygswrrqrqsvveefpfdsegptptstfsi 350

RESULT 8
AAB62389
ID AAB62389 standard; Protein; 382 AA.
AC AAB62389;
XX
DT 29-JUN-2001 (first entry)
DE Human chemokine receptor CCX CKR polypeptide.
KW Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator;
KW antiinflammatory; immunosuppressive; cytostatic; antiallergic; human;
KW immunostimulant; gene therapy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 351 /note= "encoded by TAA"
FT Misc-difference 353 /note= "encoded by TAA"
FT Misc-difference 365 /note= "encoded by TGA"
FT Misc-difference 371 /note= "encoded by TAA"
XX
PN WO200127146-A2.
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-US28067.
PR 12-OCT-1999; 99US-0159015.
PR 13-OCT-1999; 99US-0159210.
PR 20-DEC-1999; 99US-0172979.
PR 28-DEC-1999; 99US-0173389.
PR 03-MAR-2000; 2000US-0186626.
XX (CHEM-) CHEMOCENTRIX INC.
PA
PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
XX
DR WPI; 2001-281975/29.
DR N-PSDB; AAF57685.
XX
XX Isolated or recombinant chemokine receptor (designated CCX CKR)
PT polypeptide (p1) or its fragment, useful for identifying CCX CKR
PT modulators which can be used in the treatment of inflammation, allergy,
PT an autoimmune disease or cancer -
XX
PS Claim 4; Fig 1; 72pp; English.
XX
CC The invention relates to an isolated or recombinant chemokine receptor
CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,
CC SLC or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR
CC modulators. An agent that modulates the activity or expression of CCX CKR
CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR
CC -mediated condition such as inflammation, allergy, an autoimmune disease,
CC graft rejection, cancer, an infectious disease or an immunosuppressive
CC disease. The present sequence represents the human CCX CKR polypeptide.
XX
SQ Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 22; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALEQNSTDYDYEEENMGTYDYSQVELICIKEDVREFAKVLPVPLTIVFVIGLAGNS 60
Db 1 maleqngstddyeeenmgtydysqvelickedvrefakvlpvpltfivfvlagns 60
QY 61 MVVAIYAYYKKQRTKTDVYTLNLAVADLLLLFTLPWAVNAVHGWLGKIMCKITTSALYT 120
Db 61 mvvaiyayykkqrtdvyltnlavadllllftlpwavnnavhgwlgkimckitsalyt 120
QY 121 LNFVSGMQFLACISIDRYAVATKVPVPSGSGVKPCWICFCVWMAAILLSLPQLVFFYVND 180
Db 121 lnfvsqmqflacisidryavatkvpqsgvgkpcwlcfcvwmiaalilsipqlvfyvnd 180
QY 181 NARCIPFPRLYLGTSMKALIQMLEICIGFVVVPELIMGVCYFITARTLMKMPNIKISRPLK 240
Db 181 narcipfprylgtsmkalqmleicigfvvpflimgvcyfitartlmkmpnikisrplk 240
QY 241 VLLTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMKSRMDIAIQVTSIALFHSLNP 300
Db 241 vlltvvifvltqplnykvkfcraidiyslitscnmskrmdiaiqvtsialfhslnp 300
QY 301 ILYVFMGASFKNYVMKVAKYGSRRQRQSVVEFPDSEGPTPTSTFSI 350
Db 301 illyvmgaskfnyvmkvakkygswrrqrqsvveefpfdsegptptstfsi 350

RESULT 9
AAW93170
ID AAW93170 standard; Protein; 349 AA.
XX
AC AAW93170;
XX
DT 24-MAY-1999 (first entry)
DE Human HFIAO41 protein.
XX
KW HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
KW anxiety; manic depression; delirium; dementia; severe mental retardation;
KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
KW linkage analysis; gene mapping; human; ss.
XX
OS Homo sapiens.
XX
PN EP899332-A2.
XX
PD 03-MAR-1999.
XX
PF 17-FEB-1998; 98EP-0301170.
XX
PR 27-OCT-1997; 97US-0962922.
PR 15-AUG-1997; 97US-0055895.
XX
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Ellis CE;
XX
DR WPI; 1999-144803/13.
DR N-PSDB; AAX22558.
XX
PT New G-coupled receptor (HFIAO41) polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease

XX PS Disclosure; Page 25-26; 27pp; English.

XX CC This sequence encodes a G-coupled receptor, HFAO41 which is useful for

XX CC diagnosing susceptibility to diseases by detecting mutations in the

XX CC HFAO41 gene, and can diagnose diseases associated with HFAO41 protein

XX CC imbalance by determining HFAO41 polypeptide expression levels. Agonists

XX CC and antagonists of the protein can be used in treatment to activate

XX CC (agonist) or inhibit (antagonist) HFAO41 activity, in addition to direct

XX CC administration of antisense sequences to prevent expression, or HFAO41

XX CC polynucleotides to treat conditions associated with a lack of HFAO41

XX CC protein. Gene therapy may also be used to affect endogenous HFAO41

XX CC polypeptide expression. HFAO41 antibodies are useful for inducing an

XX CC immune response to immunise and prevent disease, and for isolating

XX CC HFAO41 clones or purifying the polypeptides by affinity chromatography.

XX CC HFAO41 polypeptides can be administered directly or as a vaccine to

XX CC inoculate against disease. Diseases diagnosed, prevented and treated

XX CC include bacterial, fungal, protozoan and viral infections, particularly

XX CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's

XX CC disease; acute heart failure; hypotension; hypertension; urinary

XX CC retention; osteoporosis; angina pectoris; myocardial infarction; and

XX CC asthma; allergies; benign prostatic hypertrophy; and psychotic and

XX CC neurological disorders, including anxiety, schizophrenia, manic

XX CC depression, delirium, dementia, severe mental retardation and dyskinesias

XX CC such as Huntington's disease or Gilles de la Tourette's syndrome. The

XX CC HFAO41 polypeptide is also useful for mapping the gene to a chromosome,

XX CC allowing gene inheritance to be studied through linkage analysis.

XX SQ Sequence 349 AA;

Query Match 99.7%; Score 1814; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 5.8e-195;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPFLPVFLIVFVIGLAGNSM 61
|||||
DB 1 ALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPFLPVFLIVFVIGLAGNSM 60
|||||

QY 62 VVAIVAYYKKORTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGIMCKITISALYTL 121
|||||
DB 61 VVAIVAYYKKORTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGIMCKITISALYTL 120
|||||

QY 122 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVNDN 181
|||||
DB 121 NFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVNDN 180
|||||

QY 182 ARCPIFPFRYLGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 241
|||||
DB 181 ARCPIFPFRYLGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240
|||||

QY 242 LTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 301
|||||
DB 241 LTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300
|||||

QY 302 LYVFMGASFKNYVMKVAKYGSRQRORSVEEFPDSEGPTEPTSTFSI 350
|||||
DB 301 LYVFMGASFKNYVMKVAKYGSRQRORSVEEFPDSEGPTEPTSTFSI 349
|||||

RESULT 10
AAV30125
ID AAV30125 standard; Protein; 350 AA.
XX AC AAV30125;
XX DT 14-OCT-1999 (first entry)
XX DE A human seven-pass transmembrane receptor protein.
XX KW Seven-pass transmembrane receptor; autoimmune disease;
XX KW white blood cell dysfunction.

OS Homo sapiens.
XX PN WO9933876-A1.
XX PD 08-JUL-1999.
XX PF 24-DEC-1998; 98WO-JP05886.
XX PR 24-DEC-1997; 97JP-0354537.
XX PA (ASAH) ASAH KASEI KOGYO KK.
XX PI Ishimaru H, Koshio T, Ohno T;
XX DR WPI; 1999-493806/41.
XX DR N-PSDB; AAX86674.
XX PT New seven-pass transmembrane receptor protein useful for treating,
XX PT preventing or diagnosing autoimmune diseases
XX PS Claim 1; Page 101-103; 118pp; Japanese.
XX CC The present sequence represents a seven-pass transmembrane receptor
XX CC protein. The protein and its DNA can be used to screen substances
XX CC for the diagnosis, prevention and treatment of autoimmune diseases,
XX CC particularly those due to white blood cell dysfunction.

SQ Sequence 350 AA;

Query Match 99.7%; Score 1814; DB 20; Length 350;
Best Local Similarity 99.7%; Pred. No. 5.8e-195;
Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPFLPVFLIVFVIGLAGNS 60
|||||
DB 1 MALEQNQSDYYEENMGTYDYSOYELICIKEDYREFAKVPFLPVFLIVFVIGLAGNS 60
|||||

QY 61 MVVAIVAYYKKORTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGIMCKITISALYTL 120
|||||
DB 61 MVVAIVAYYKKORTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGIMCKITISALYTL 120
|||||

QY 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
|||||
DB 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFTVND 180
|||||

QY 181 NARCPIFPFRYLGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240
|||||
DB 181 NARCPIFPFRYLGTSMKALIQMLEICIGFVWPFLINGVCYFITARTLMKMPNIIKISRPLK 240
|||||

QY 241 LTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300
|||||
DB 241 LTVVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSLNPI 300
|||||

QY 301 ILYVFMGASFKNYVMKVAKYGSRQRORSVEEFPDSEGPTEPTSTFSI 350
|||||
DB 301 ILYVFMGASFKNYVMKVAKYGSRQRORSVEEFPDSEGPTEPTSTFSI 350
|||||

RESULT 11
AAV71301
ID AAV71301 standard; Protein; 350 AA.
XX AC AAV71301;
XX DT 02-NOV-2000 (first entry)
XX DE Human orphan G protein-coupled receptor hPPR1.
XX KW Human; orphan G protein-coupled receptor; GPCR; hPPR1; drug screening;
XX KW transmembrane receptor; expressed sequence tag; EST; signal cascade.

OS Homo sapiens.

PT Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents -
PS Example 1; Page 99-100; 187pp; English.
XX
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AA446017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
XX

SQ Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;
Best Local Similarity 99.4%; Pred. No. 1.6e-194;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MALEQNSTDYEEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
Db 1 maleqnqstdyeeenemngtydysqyelickedvrefakvflpvfltiafviglagns 60
Qy 61 MVVAIYAYKKQRTDVIYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
Db 61 mvvalyayykkqrtkdviylnlavaddlllftlpfwavnavhgvlgkimgckitsalyt 120
Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVKPCWICFCVWMAAILLSIPQLVFTVND 180
Db 121 lfnvsgmqflacisidryvavtnvpsqsgvqgkpcwlicfcvwmaaillspqlvftvnd 180
Qy 181 NARCIPPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
Db 181 narcipifprylgtsmkaligmeicigfvpflmgvcyftartlmkmpnikisrplk 240
Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDDIAIQVTESIALFHSCLNP 300
Db 241 vlltvvifvltqlpynivkfcraidiislylitscnmskrmdiaiqvtesialfhsclnp 300
Qy 301 ILYVPMGASFKNYVMKAKKYGSRQRQSVSEFFPDSGPTPTSTFSI 350
Db 301 ilyvfmgasfknymkvakkygswrrqrsveefpdsgeptptstfsi 350

RESULT 13

AAB37788
ID AAB37788 standard; Protein: 350 AA.

XX AC AAB37788;

DT 23-FEB-2001 (first entry)

XX DE Human TSC7.

KW Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial;
KW osteopathic; antiulcer; antiasthmatic; antiallergic; neuroprotective;
KW cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;
KW analgesic; tranquiliser; immunosuppressive; antiinflammatory;
KW gene therapy; TSC7; infection; cancer; autoimmune disorder;
KW Parkinson's disease; osteoporosis; neurological disorder.

XX OS Homo sapiens.

XX PN WO2000064941-A2.

XX PD 02-NOV-2000.

XX PF 21-APR-2000; 2000WO-US10979.

XX PR 23-APR-1999; 99US-0130817.

PR 20-APR-2000; 2000US-0556002.

XX PA (CURA-) CURAGEN CORP.

XX PI Gould-Rothberg BE;

XX XX

DR WPI; 2000-679670/66.

DR N-PSDB; AAC68722.

XX Novel nucleic acid encoding G-protein coupled receptor for diagnosis
XX and treatment of conditions associated with disorder in a G-protein
XX mediated pathway such as cancer, neurological disorders and infections

PS Claim 12; Page 8; 132pp; English.

XX XX

CC The present sequence is human tuberous sclerosis complex 7 (TSC7).
CC TSC7 polynucleotides and polypeptides are useful for determining the
CC presence or predisposition to a disease associated with altered levels of
CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the
CC polypeptide are useful for treating or preventing pathological conditions
CC associated with the disorder in a G-protein mediated pathway. They are
CC useful for diagnosing a hyperproliferative condition such as a neoplasm
CC or dermatological condition. TSC7 nucleic acids and polypeptides are
CC useful in the treatment of microbial infections, pain, cancer, anorexia,
CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,
CC hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy
CC and psychotic and neurological disorders, including schizophrenia,
CC dementia, severe mental retardation and dyskinesias, such as
CC Huntington's disease and/or other pathologies and disorders. TSC7
CC polypeptides are also useful as immunogens to produce antibodies and as
CC vaccines.

SQ Sequence 350 AA;

Query Match 99.4%; Score 1808; DB 21; Length 350;
Best Local Similarity 99.4%; Pred. No. 2.7e-194;
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALEQNSTDYEEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60

Db 1 maleqnqstdyeeenemngtydysqyelickedvrefakvflpvfltiiviglagns 60

Qy 61 MVVAIYAYKKQRTDVIYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120

Db 61 mvvalyayykkqrtkdviylnlavaddlllftlpfwavnavhgvlgkimgckitsalyt 120

Qy 121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVKPCWICFCVWMAAILLSIPQLVFTVND 180

Db 121 lfnvsgmqflacisidryvavtnvpsqsgvqgkpcwlicfcvwmaaillspqlvftvnd 180

Qy 181 NARCIPPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240

Db 181 narcipifprylgtsmkaligmeicigfvpflmgvcyftartlmkmpnikisrplk 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDDIAIQVTESIALFHSCLNP 300

Db 241 vlltvvifvltqlpynivkfcraidiislylitscnmskrmdiaiqvtesialfhsclnp 300

Qy 301 ILYVPMGASFKNYVMKAKKYGSRQRQSVSEFFPDSGPTPTSTFSI 350

Db 301 ilyvfmgasfknymkvakkygswrrqrsveefpdsgeptptstfsi 350

RESULT 14

AAY57289

ID AAY57289 standard; Protein: 333 AA.

XX AC AAY57289;

XX DT 05-JUN-2000 (first entry)

```
XX DE Human BGCR partial amino acid sequence.
XX BGCR protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX OS Homo sapiens.
XX PN WO9952945-A2.
XX PD 21-OCT-1999.
XX PF 16-APR-1999; 99WO-US08395.
XX PR 16-APR-1998; 98US-0061753.
XX PR 16-APR-1999; 99US-0061753.
XX PA (MILL-) MILLENIUM PHARM INC.
XX PI Gonzalo JA, Gutierrez-Ramos JC;
XX WPI; 1999-620375/53.
XX DR N-PSDB; AAZ90527.
XX PT New nucleic acid encoding human BGCR receptor, used e.g. for
XX modulating inflammation and tumor growth.
XX PS Claim 1; Fig 1A-B; 123pp; English.
XX The invention relates to a human BGCR protein, a G-protein coupled
CC receptor. The BGCR protein can be expressed by standard recombinant
CC methodology. BGCR are receptor proteins possibly involved in modulation
CC of proinflammatory or stimulatory functions of chemokines; cell
CC proliferation, migration, adhesion and targeting, and exocytosis. The
CC BGCR nucleic acids and derived proteins (or their variants), antibodies
CC and modulators are potentially useful for modulating inflammation;
CC chemotactant activity of leucocytes; angiogenesis; cell proliferation;
CC tumour growth; allergic reactions and entry of human immune deficiency
CC virus into cells, for therapeutic or prophylactic purposes. They are also
CC used for diagnosis and in drug-screening assays. The present sequence
CC represents the sequence of a partial human BGCR protein.
XX SQ Sequence 333 AA;
XX
XX Query Match 95.0%; Score 1728; DB 20; Length 333;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-185;
XX Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 MNGTYDYSQVELICIKEDVREFAKVLPVLTIVFVIGLAGNSMVAIYAYKKQRTKTD 77
DB 1 mngtydysqvelicikedvrefakvlpvltivfiviglagnsmvaiyaykkqrktkd 60
QY 78 VYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALYTLNFSVGMQFLACISIDR 137
DB 61 vyilnlavaddlllftlpfwavnavhgwlgkimckitsalyltnfsvgmqflacisidr 120
QY 138 YVAVTKVPSSGVGKPCWICFCVWMAAILLSIPQLVFTVNDNARCIPIFPRLVGTSMK 197
DB 121 yvavtkvpssgv9gkpcwlcfcvwm aailslpqlvftvndnarcipifprylgtsmk 180
QY 198 ALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNLIKSRPLKVLNFWIVFVITQLPYN 257
DB 181 aliqmlaicigfvvpflimgvcyfitartlmkmpniksrplkvlntwivfvtqipy 240
QY 258 IVKFCRAIDIIYSLITSCNMSKMDIAOVTESALPHSCINPLTYVFMGSFKNYVMKV 317
DB 241 ivkfcraidl iyslitscnmskmdiaqvtesialfhsclnpltyvfmgsfknymkv 300
QY 318 AKKYGSRQRQSVSEEPFDSGTEPTSTFSI 350
DB 301 akkygswrrqrqsvseefpdsgeptstfsi 333
```

RESULT 15

AAG67238

ID AAG67238 standard; Protein; 350 AA.

XX

AC AAG67238;

XX

DT 13-NOV-2001 (first entry)

XX

DE Amino acid sequence of bovine chemokine receptor CCR11.

XX

KW Human; chemokine receptor; CCR11; G protein coupled receptor;
KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; arteriosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction; migraine; preterm labour;
KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosis;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

XX OS Bos sp.

XX

XX WO200166598-A2.

XX

XX 13-SEP-2001.

XX

XX 05-MAR-2001; 2001WO-US07073.

XX

XX 03-MAR-2000; 2000US-0186928.

XX

XX 03-MAR-2000; 2000US-0187231.

XX

XX (ICOS-) ICOS CORP.

XX

XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;

XX

XX WPI; 2001-541918/60.

XX

XX N-PSDB; AAH77712.

XX

An isolated polynucleotide encoding the chemokine receptor CCR11,
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiogenesis, arteriosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine.

XX

XX Example 1; Page 99-100; 110pp; English.

XX

The present sequence represents the bovine chemokine receptor CCR11.
CCR11 is a member of the G protein coupled receptor family. A CCR11
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
CC expression or biological activity, is useful for treating many
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
CC bowel disease, and asthma. They are also useful for treating
CC angiogenesis, arteriosclerosis vascular association diseases which may
CC include but are not limited to hypertension, angina pectoris, cardiac
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
CC pulmonary vascular disease.

XX

SQ Sequence 350 AA;

Query Match 89.1%; Score 1620; DB 22; Length 350;

Best Local Similarity 86.0%; Pred. No. 3.5e-173;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALQNSTDYDYENENMNGTYDYSQVELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60

DB 1 maveyngstdydyeenenmdthdysqvelicikeevrfakvlpafvtiafiaglns 60

QY 61 MVVAIYAYKKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGWLGKIMCKITSALY 120

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Result No.	Score	%			ID	Description
		Query Match	Length	DB		
1	1596	87.7	350	11	Q924T3	Q924I3 mus musculus
2	912	50.1	221	11	Q9ESK1	Q9eskl rattus norv
3	643	35.3	369	4	Q9UQQ6	Q9uqq6 homo sapien
4	611	33.6	367	11	Q9R1V0	Q9riv0 mus musculus
5	586.5	32.2	368	13	Q42444	Q42444 oncorhynchus
6	578	31.8	343	6	Q9N0Z0	Q9n0z0 cercocebus
7	566.5	31.1	351	11	Q9E0I6	Q9eqi6 mus musculus
8	566	31.1	343	6	Q9BDS6	Q9bds6 macaca fasc
9	561.5	30.9	351	11	Q9ERH5	Q9erh5 mus musculus
10	560	30.8	342	4	Q9HCAS	Q9hcas homo sapien
11	559	30.7	342	6	Q9TV16	Q9tv16 pan troglod
12	544	29.9	358	13	Q9PUA0	Q9puao acipenser r
13	534.5	29.4	360	11	Q91ZH4	Q91zh4 rattus norv
14	527	29.0	384	4	Q96A02	Q96a02 homo sapien
15	520.5	28.6	358	13	Q9YG33	Q9ygc3 xenopus lae
16	516	28.4	355	11	Q9JLY8	Q9jly8 rattus norv

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QY 181 NARCIPFPRLYLGTSKALIQMLEICIGFVFPFLINGVYFITTARTLTKMKNPKIKSRPLK 240
DB 181 NARCTPIFFPHHLGTSKASIQMLEIGFVFPFLINGVYASTARALIKMKNPKIKSRPLR 240
QY 241 VLLTVVIVFIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTSIALFHSCLNP 300
DB 241 VLLAVVVFIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTSIALFHSCLNP 300
QY 301 ILYVFMGASFKNVYKVAKYGSRWRQSRQSEFFPDSEGPTEPTSTFSI 350
DB 301 ILYVFMGASFKNVYKVAKYGSRWRQSRQSEFFPDSEGPTEPTSTFSI 350
RESULT 2
ID Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1.
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE PUTATIVE G-PROTEIN COUPLED RECEPTOR GPCR14 (FRAGMENT).
GN GPCR14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RL receptors expressed in regenerating peripheral nerve.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090348; AAG24470.1; .
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match 50.1%; Score 912; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 3,9e-73;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FVAVNAVHGVWLGKIMCKITSALYTLNFSVGMQFLACISIDRYAVATKVPQSGVGKPCW 155
DB 19 FVAVNAVHGVWLGKIMCKITSALYTLNFSVGMQFLACISIDRYAVATKVPQSGVGKPCW 78
QY 156 IICFCVWMAAILLSIPQLVFTVNDNARCIPIFPRLYLGTSKALIQMLEICIGFVFPFLI 215
DB 79 IICCCVWMAAILLSIPQLVFTVNDNARCIPIFPRLYLGTSKALIQMLEICIGFVFPFLI 138
QY 216 MGVCYFITTARTLTKMKNPKIKSRPLKLVLLTVVIVTQLPNIVKFCRAIDIIYSLTSC 275
DB 139 MGVCYAMTARKLTKMKNPKIKSRPLRLVAVVVFIVTQLPNIVKFCRAIDIIYSLTSC 198
QY 276 NMSKRMIDIAIQVTSIALFHSCL 298
DB 199 DMSKRMIDIAIQVTSIALFHSCL 221

RESULT 3
Q9UQ06
ID Q9UQ06 PRELIMINARY; PRT; 369 AA.
AC Q9UQ06.
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)

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DT 01-OCT-2001 (TremBLrel. 18, Last annotation update)
DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RL receptor for the chemokine TECK.";
RL J. Immunol. 162:5671-5675(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RL 15).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; .
DR EMBL; AF145439; AAF66699.1; .
DR InterPro; IPR004069; Chemokine9_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 369 AA; 42015 MW; F27CEA0CFB6B844C CRC64;

Query Match 35.3%; Score 643; DB 4; Length 369;
Best Local Similarity 36.4%; Pred. No. 4.5e-49;
Matches 120; Conservative 75; Mismatches 117; Indels 18; Gaps 4;

QY 6 NQSTDYEE-NEMNGTYDYSQYELICIKEDYREFAKVLPVLTIVFVIGLAGNSMVA 64
DB 12 NMADDYSESTSMEDYVNFNFTDFYCEKNVRQFASHFLPPLYLWLVFVIGALGNSLVL 71
QY 65 IYAYYKQRTKTDVYLLNLAVALDLLLFTLPFVAVNAVHGVWLGKIMCKITSALYTLNFV 124
DB 72 VYVYCTRVKTMDFLLNLAIALDLFLVLPFMAIAAADQWKFQTFMCKVWNSYKMFY 131
QY 125 SCMOFLACISIDRYAVATKVPQSGVGKPCW-----IICFCVWMAAILLSIPQLV 175
DB 132 SCVLLIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKMVCFTIWLAAALCIPEILY 186
QY 176 YTVNDN---ARCIPIFPRLYLGTSKALIQMLEICIGFVFPFLINGVYFITTARTLTKMKN 232
DB 187 SQIKESGIAICTWVYPSDESTKLSAVLTKVLGFFLPFVVMACCYTIIHTLIQAKK 246
QY 233 IKISRLPKVLLTVVIVTQLPNIVKFCRAIDIIYSLTSCNMSKRMIDIAIQVTESTA 292
DB 247 SKHKALKKTIITVLTIVFVLSQFPYCNILLVQTDIYAFMISCAVSTNIDICFQVTQTTA 306
QY 293 LFHSCNLPILYVFMGASFKNVYKVAKYG 322
DB 307 FPHSCNLPILYVFMGASFKNVYKVAKYG 336

RESULT 4
Q9R1V0
ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0.
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT 9
Q9ERH5 PRELIMINARY; PRT; 351 AA.
AC Q9ERH5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN CXCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=SPLEEN;
RA Sato H., Taniguchi M.;
RT "Molecular cloning of a putative chemokine receptor preferentially
RT expressed in mouse lymphocytes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF305709; AAG31284.1; -.
DR MGD; MGI:1934582; CXCR6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40511 MW; B00E3134D2B4D1ED CRC64;

Query Match 30.9%; Score 561.5; DB 11; Length 351;
Best Local Similarity 35.4%; Pred. No. 7e-42;
Matches 127; Conservative 69; Mismatches 126; Indels 37; Gaps 10;

QY 10 DYIYEE--EMGTGYDYSOYELICIKEDV--EFAKVFLPVLTVFVIGLAGNSMVAI 65
DB 12 DGHYEGDFLWNSSDNSQ-----ENRFLKFEVFLPCVLYVVFVGLLGNLSVLII 64
QY 66 YAYKKORTDVTILNLAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLNLFVS 125
DB 65 YIFYOKRLTDFVLNLPLADLVFCTLPFWAYAGTIEWVFGTVMCKTLRGMYTNFVY 124
QY 126 GMQFLACISIDRYAV--TKVPSOSGVGKPCW--IICFCVWMAALLSIPQLVFTVND 180
DB 125 SMLTLCITVDREIVVQATKAFNRQAKW-IWQVVICLLIWWVSLVSLPQLIYGHVQD 183
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGVVPFLMGVCYFITARTLMKMPNIIKISRPLK 240
DB 184 IDKLI---CQYHSEESTMVLVIQMTGFFLPPLTLMILCYSGIITLLHARNFQKHSLK 240
QY 241 VLLTVVIVFIVTQPNVIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
DB 241 IIFLVAVFLLQTQTFNLAMLQSTSWEYTTTS-----FKYIVVTEAIAIFRACLNP 294
QY 301 ILYVFMGASFKNYVAKVKKY-----SWRRQOSVEEFPDSEGTPTSTFSI 350
DB 295 VLYAFVGLKFRKNVWKLMDIGCLSHLGVSQWKSSDSK--TCSASHNVETTSFMQL 351

RESULT 10
Q9HCA5 PRELIMINARY; PRT; 342 AA.
AC Q9HCA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MUTANT G PROTEIN-COUPLED RECEPTOR STRL33.
GN STRL33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (BOB).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -.

Query Match 30.8%; Score 560; DB 4; Length 342;
Best Local Similarity 33.1%; Pred. No. 9.3e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YYEENEMGTGYDYSOYELICIKEDVREFAKVFLPVLTVFVIGLAGNSMVAIYAYKK 71
DB 6 YHEDYGFSSFNDSQBE---HODELQFSKVFLPCVLYVVFVGLGNSLVLSIFPYHK 61
QY 72 QRTKTDVYILNLAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLNLFVSGMOFLA 131
DB 62 LQSLTDVFLVNLPLADLVFCTLPFWAYAGIHEWVFGVQVCKSLGIIYTLNFTSMILT 121
QY 132 CISIDRYAVATKVP--QSGVGKPCW--IICFCVWMAALLSIPQLVFTV--NDNRCI 185
DB 122 CITVDREIVVQATKAFNRQAKW-IWQVVICLLIWWVSLVSLPQLIYGHVQD 180
QY 186 PIPRYLGTSMKALIQMLEICIGVVPFLMGVCYFITARTLMKMPNIIKISRPLKLLTV 245
DB 181 ----GYHDEAISTVLTATQMTGLFPLTMIVCYSVIITLLHAGGFQKHSUKIIFLV 236
QY 246 VIVFIVTQPNVIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNPILYVF 305
DB 237 MAVFLLTQTFNLAMLQSTSWEYTTTS-----IMVTEAIAIFRACLNPVLYAF 290
QY 306 MGASFKNYVAKVKKY-----SWRRQOSVEEFPDSEGTPTSTFSI 350
DB 291 VSLKFRKNFWKLMDIGCLPGLGVSHQWKSSDSK--TFSASHNVETTSFMQL 342

RESULT 11
Q9TV16 PRELIMINARY; PRT; 342 AA.
AC Q9TV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (BOB).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=973111099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1.";
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=SPLEEN;
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029759; AAG21918.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39279 MW; CE149633D01D20AA CRC64;

Query Match 30.8%; Score 560; DB 4; Length 342;
Best Local Similarity 33.1%; Pred. No. 9.3e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

QY 12 YYEENEMGTGYDYSOYELICIKEDVREFAKVFLPVLTVFVIGLAGNSMVAIYAYKK 71
DB 6 YHEDYGFSSFNDSQBE---HODELQFSKVFLPCVLYVVFVGLGNSLVLSIFPYHK 61
QY 72 QRTKTDVYILNLAVADLLLTLPFWAVNAVHGVGLGKIMCKITSALYTLNLFVSGMOFLA 131
DB 62 LQSLTDVFLVNLPLADLVFCTLPFWAYAGIHEWVFGVQVCKSLGIIYTLNFTSMILT 121
QY 132 CISIDRYAVATKVP--QSGVGKPCW--IICFCVWMAALLSIPQLVFTV--NDNRCI 185
DB 122 CITVDREIVVQATKAFNRQAKW-IWQVVICLLIWWVSLVSLPQLIYGHVQD 180
QY 186 PIPRYLGTSMKALIQMLEICIGVVPFLMGVCYFITARTLMKMPNIIKISRPLKLLTV 245
DB 181 ----GYHDEAISTVLTATQMTGLFPLTMIVCYSVIITLLHAGGFQKHSUKIIFLV 236
QY 246 VIVFIVTQPNVIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTESIALFHSCLNPILYVF 305
DB 237 MAVFLLTQTFNLAMLQSTSWEYTTTS-----IMVTEAIAIFRACLNPVLYAF 290
QY 306 MGASFKNYVAKVKKY-----SWRRQOSVEEFPDSEGTPTSTFSI 350
DB 291 VSLKFRKNFWKLMDIGCLPGLGVSHQWKSSDSK--TFSASHNVETTSFMQL 342
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DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match
Best Local Similarity 30.7%; Score 559; DB 6; Length 342;
Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;

QY 12 YEEENMGTYDYQYSELICIKEDVREFAKVPFLVTFVIGLAGNSMVAIYAYKK 71
DB 6 YHEDYGFNSFSSQEE---HQDFLOFSKVPFLPCMYLVFVCGLVNSLVLSIFHYK 61

QY 72 QRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTFVSGMOFLA 131
DB 62 LQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGVMCKSLGIYINFTSMILIT 121

QY 132 CTSIDRYAVAVTKPS--QSGVGKPCW--IICFCVYMAAILLSIPOLVFTV--NDNARCI 185
DB 122 CTVDRFIVVVKATRAYNOQAKRWGKVTSLIWIYSLVSLPQIIYGNVFNLDKLC- 180

QY 186 PIPPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNKRISRLKVLTV 245
DB 181 ----GYHDEAISTVVLATQMTLGFLLTMTIVCVSVIITKLLHAGGFQKHRSKLIIFLV 236

QY 246 VIVFIVTQLPYNIIVFCRAIDIIYSLITSCNMSKRMDAIOVTESIALPHSCINPLIYVF 305
DB 237 MAVFLITQMPFLNKLIRSTHWEYATMSFHYT-----IMTEATAYLRACLNPLYAF 290

QY 306 MGASEFKNYVMKAKYKG-----SWRRQSQVEEPFDEGPEPTSTFSI 350
DB 291 VSLKFKNKWKLVDIGCLPYLGVSQHWKSSSEDNSK--TFSASHNVVATSMFQL 342

RESULT 12
Q9PUA0 PRELIMINARY; PRT; 358 AA.
AC Q9PUA0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4.
GN CXC4.
OS Acipenser ruthenus (sterlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenserinae; Acipenser.
OX NCBI_TaxID=7906;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368347; PubMed=10906389;
RA Alabyev B.I., Najakshin A.M., Mechetina L.V., Taranin A.V.;
RT "Cloning of a CXC4 homolog in chondrosteian fish and characterization
of the CXC4-specific structural features.";
RL Dev. Comp. Immunol. 24:765-770(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ249438; CAB60252.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40448 MW; 7B3B99B962453008 CRC64;

Query Match
Best Local Similarity 29.9%; Score 544; DB 13; Length 358;
Matches 117; Conservative 74; Mismatches 131; Indels 32; Gaps 8;
```

```
Matches 125; Conservative 64; Mismatches 145; Indels 18; Gaps 7;

QY 8 STDYEEEN-EMNGTYDYQYSELICIKEDVREFAKVPFLVTFVIGLAGNSMVAIY 66
DB 7 TVDFTFENNTGSGDYSQYDEVCKRNLDGRKIFLPTVYTIIFVMGIVGGLVIVM 66

QY 67 AYYKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTFVSG 126
DB 67 G-YQVKWTMDKYRLHLLIADLFLVTFLPFWADAAASSWTFGGFLCKIYINVLNLYSS 125

QY 127 MQFLACISIDRYAVAVTKPSQSGVKPC-----WIICFCVYMAAILLSIPOLVFTYNDN 181
DB 126 VLTLAFISFDRLAVVVRATNSH---KPRKLAERKIIYVGVVLPATLLTVDFLFAQVHDE 182

QY 182 A---RCIPFIPRVLGTSMKALIQMLEICIGFVVPFLMGVCYFITARTLMK-MPNTKISR 237
DB 183 GTRMCDRVPYSGSGNIMWTIFRFOHIFVGLVPLGLVILTCYCIITIKLSQSGSKGLQKR 242

QY 238 PLKVLTVVIVFTVTPYNIIVFCRAIDIIYSLITSCNMSKRMDAIOVTESIALPHSC 297
DB 243 ALKTTIILAFICWLPYCIALVDLTVLLNVIQYNCTLOHMETWIFVTEGLAYPHCC 302

QY 298 LNPILVFMGASPKNYVMKAKYKGSRRQSQVEEPFDEGPEPTSTFS 349
DB 303 LNSILYAFLGKVPK----KSAKSALTVNSRSGSLKILSKNKGGLSSVSTES 350

RESULT 13
Q91ZM4 PRELIMINARY; PRT; 360 AA.
AC Q91ZM4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW;
RA Garcia G.E., Chen S., Xia Y., Harrison J., Willson C.B., Johnson R.J.,
RA Bacon K.B., Feng L.;
RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
chemokine results in attenuation of developing crescentic
glomerulonephritis.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432872; AAL30398.1; -.
KW Receptor.
SQ SEQUENCE 360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 11; Length 360;
Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;

QY 3 LEQNQSTDYEEENMGTYDYQYSELICIKEDVREFAKVPFLVTFVIGLAGNSMW 62
DB 1 MNATEVDTTQDTEYNSYFDESPLPKCTKEGIRAFGEVFLPPLYSLVFLGLFGNSV 60

QY 63 VAIYAYYKQRTKTDVYILNLAVALDLLLFTLPFWAVNAVHGVLGKIMCKITSALEYTF 122
DB 61 VLVLFKYRLKSMTDVYLLNLAISDLLFVLSLPFGWYAADQWVFLGLCKITSMWLVG 120

QY 123 FVSGMOFLACISIDRYAVAVTKV-----PSQSGVKPCWIIICFCVYMAAILLSIPOLVF 175
DB 121 FYSGFIIFMLSIDRYLAIVHAVFSLRARTLTGV-----ITSLITWSVAVFASLPGLLF 175

QY 176 YTV---NDNARCIPFIPRVLGTSMKALIQMLEI-CIGFVVPFLMGVCYFITARTLMKMP 231
DB 176 STCDTENNHITYCKTQYS--VNSTTWKVLSSLEINLGLVILPLGIMLFCYSMIITLRHCK 233
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:05:40 ; Search time 17.74 Seconds
(without alignments)
1895.787 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONQSTDYEEENEMNG.....VEEFPDSEGTPTSTFSI 350
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	89.1	350	JN0621	G protein-coupled
2	659	36.2	378	B55735	lymphocyte-specifi
3	650	35.7	378	A55735	G protein-coupled
4	643	35.3	378	A45680	G protein-coupled
5	583	32.1	369	JC5088	G protein-coupled
6	537.5	29.5	360	A57160	chemokine (C-C) re
7	534.5	29.4	360	A53611	interleukin-8 rece
8	524	28.8	354	158186	probable G protein
9	523.5	28.7	355	JC4304	orphan G protein-c
10	522.5	28.7	360	JC4587	chemokine (C-C) re
11	518.5	28.5	354	A55733	G protein-coupled
12	511	28.1	358	A53752	interleukin-8 rece
13	501.5	27.6	355	JQ1231	neuropeptide Y/pep
14	500.5	27.5	352	A45747	neuropeptide Y/pep
15	499.5	27.5	353	J28787	neuropeptide Y/pep
16	493.5	27.1	352	G00048	fusin (LESTRA) - c
17	492	27.0	360	JC2443	chemokine (C-C) re
18	489.5	26.9	350	A39445	interleukin-8 rece
19	486	26.7	355	JC5067	G protein-coupled
20	485	26.7	355	J49339	macrophage inflam
21	484.5	26.6	352	A43113	chemokine (C-C) re
22	483.5	26.6	359	A48921	interleukin-8 rece
23	482	26.5	374	I38450	chemokine (C-C) re
24	479.5	26.4	359	I49341	MIP-1 alpha recept
25	476.5	26.2	367	JE0349	interferon-inducib
26	474	26.1	355	A45177	chemokine (C-C) re
27	471	25.9	356	S42096	interleukin-8 rece
28	470	25.8	383	S55594	G protein-coupled
29	461.5	25.4	355	G02436	chemokine (C-C) re

ALIGNMENTS

RESULT 1
JN0621
G Protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C:Accession: JN0621
R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
A:Reference number: JN0621; MUID:93326166
A:Accession: JN0621
A:Molecule type: mRNA
A:Residues: 1-350 <MAT>
A:Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
A:Experimental source: tongue taste papillae
C:Comment: This protein is involved in modulating taste sensitivity or regeneration o
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F:42-66/Domain: transmembrane #status predicted <TM1>
F:80-99/Domain: transmembrane #status predicted <TM2>
F:114-135/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>
F:200-222/Domain: transmembrane #status predicted <TM5>
F:242-265/Domain: transmembrane #status predicted <TM6>
F:284-306/Domain: transmembrane #status predicted <TM7>
F:6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	89.1%	Score 1620;	DB 2;	Length 350;
Best Local Similarity	86.0%	Pred. No. 1.1e-131;		
Matches 301;	Conservative 27;	Mismatches 22;	Indels 0;	Gaps 0;
Qy	1	MALEONQSTDYEEENEMNGTYDSOYELICIKEDVREFAKVLPLVFLVIFVIGLAGNS	60	
Db	1	MAVEYNQSTDYEEENEMNDTHDSQYEVICIKKEEYFAKVLPAFFTAFTIGLAGNS	60	
Qy	61	MVAIVAYVKKORTDVYILNLAVADLLFTLPFWAVNAVHGVGLGIMCKITSAVLT	120	
Db	61	TVVAIVAYVKKRTKDVYILNLAVADLLFTLPFWAVNAVHGVGLGIMCKVTSALYT	120	
Qy	121	LNFSVGMQFLACISIDRYVAVTVKPSQSGVGRKPCWICFCVWMAAILLSIPQLVFTVND	180	
Db	121	VNFVSGMQFLACISIDRYVAVTVKAPSQSGVGRKPCWICFCVWVAAILLSIPQLVFTVNH	180	
Qy	181	NARCIPIPPRYLGTSMKALIQMLEICIGRVDFLNGVCYFTARTLMKNPKIKSRPLK	240	
Db	181	KARCVPIFPYHLGTSMKASIQILEICIGFIIPFLINAVCYFITAKTLIKMPNKKSQPLK	240	
Qy	241	VLLTVVIVFIVTQLPVNIYVKFCRADIIYSLITSCNMSKRMIDIAIOVTESIALFHSLNP	300	
Db	241	VLFVTVVIVFIVTQLPVNIYVKFCQADIIYSLITDCMSKRMIDVAIQITESIALFHSLNP	300	

[illegible]

RESULT 7
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37898; I38712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for h
A:Reference number: I37898; MUID:95014476

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U11801; PID:g511803
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873;
U11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID:
R;Sprengrer, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Keivin, D.J.
I Biol Chem 260:11465-11470, 1985

A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown

A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL9RA, binds several peptides besides interleukin-8, in
C:Genetics:
A:Gene: GDB:IL9RB; IL9RA
A:Cross-references: GDB:I27868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.4%; Score 534.5; DB 2; Length 360;
Best Local Similarity 33.3%; Pred. No. 2.1e-38;
Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

QY QY
LEQNOSTDYVEENEMNCTDYSQVELI-----CIKEDVREFAKFLPVFLTIVFVLGA 57
MFSGSGEDEFNFACPY GNVVCXCGCFCPCFY KALBGGCCG CCCCCCCC

58 GNSMVVAIYAYKKQRTKTDVYILNLAVADLLFLPFWAVNAVHGVLGKIMCKITSA 117
|||:: : | : |||::|||::||| :|||:: :|||:: :|||:: :
65 GNSLYMLVILYSRVGRSTVDYLLNLADELFAULTPLPIWAASKVNGWIFGTFLCKVWSL 124

```

118 LYTNFVSGMQFLACISIDRYVAV---TKVPSQSGVGKPCWICFCVWMAAILLSIPQLV 174
      | :| | | | :| | | | | :| :| :| :| | | | :|
125 LKEVNFVSGTLLACISVDYRLAIYHVTLTQRRY---LVKFICLSIWGSLSLALPVLV 182

```

db 125 LKEVNFYSGILLACISVDRYLAIVHATRLTQKRY--LVKFICLSIWGLSLLALPVL 182

[illegible]

RESULT 8

I58186
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I58186
R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spin
A:Reference number: I58186; MUID:94323113
A:Accession: I58186
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 28.8%; Score 524; DB 2; Length 354;
Best Local Similarity 36.9%; Pred. No. 1.7e-37;
Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps 4;

QY 22 YDYSQYELICIKEDVREFAKVFLVFLTIVFVIGLAGNSMWVAIYVYKKQRTKTDVYIL 81
 DB 13 FEYNDQSAFVLCNIVACCTIETI STEVET VETDREVCNTI EYET AT MVQDQVQVCTQVET 79

[illegible]

DS 73 NDAISDLLEFVAIDFWTHYLISHEGLHNAMCKLTATFAFFGFFGGFFITVISIDRYLAI 132

QY 142 TKVPS-----QSGVGKPCWIIICFCVWMAAILISIPQLVFYTVVNDNARCIPFPFVLGT 194

Db 133 VLAANSMNRTVQHGV----TISLGVAAAILVASPQFMFTKKRDN-ECUGSDYPEVLQE 186

QY 195 SMKALIQMLEICIGFVVPFLINGVCYFITTALMKMPNIKISRPLKVLTTWVIIVFTQL 254

Db 187 IMPVLNRSEVNILGEVLPILLMSFCYFRIVRTLFSCNRRKKARAILLILVVVVFFLWT 246
QY 255 PYNIWKFCAIDIIYSLITSCNMKSRMDIAQTQVTESTALFHSCLNPILYVFMGASFKNVY 314

Db	247	PYNIVFLETLK-FYNFPSCMKRDLRWALSVTETVAFSHCCLNPIYAFAGEKFRYL	305
Oy	315	MKVAKK	320

Db 306 RHLYNK 311

RESULT 9
JC4304
orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304

R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 293-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi
A:Reference number: JC4304; MUID:96011651
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U03050; NID:9665580; PIDN:AAA91783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C:Comment: This protein is a key regulator of many immune and homeostatic responses, and
C:Genetics:
A:Gene: v28
A:Map position: 3pter-p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-98/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 28.7%; Score 522.5; DB 2; Length 355;
Best Local Similarity 36.4%; Pred. No. 2.3e-37;
Matches 112; Conservative 57; Mismatches 122; Indels 17; Gaps 5;
QY 22 YDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMWVAIYKKQRTKTDVIL 81
DB 12 FEYDDLAECYIGDIVVFGVIFSIYSVIFAIGLVGNLLVAFALNSKKPKSVTDIYL 71
QY 82 NLAVADLLFTLPFWAVNAVHGWIGKIMCKITSALTYLNEFSGMQLACISIDRVAV 141
DB 72 NLASDLLFVATLPFWTHYLINKEGLHNAMCKTFTAFFGFGSIFFIIVISIDRLAI 131
QY 142 TKVPS-----QSGVGKPCWICFCVWMAAILLSIPQLVFTVNDNARCIPIPRYLGT 194
DB 132 VLAANSNNRTVQGV-----TISLGWMAAAILVAAPQFMFTOKEN-ECLGDYPEVLQE 185
QY 195 SMKALIQMLEICIGFVVPFLMGVCFITARTLKMKNISRLPKLVLLTVVIVFIQTOL 254
DB 186 IWPVLARVETNFGLFGLPLLLINSYCFRIQTFLFSCNKHKKAKAUKILLVIVFFLFWT 245
QY 255 PYNIVAFCAIDIIYSILTSNCKSKRMIDIAIQVTESTIALFHSCLNPLIYVFMGASFKNYV 314
DB 246 PYNVMIFLETLK-LYDFFPSCDKRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRYL 304
QY 315 MKVAKYK 322
DB 305 YHL---VG 309

RESULT 10
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus

F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status p
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi
Query Match 28.7%; Score 522.5; DB 2; Length 360;
Best Local Similarity 33.7%; Pred. No. 2.3e-37;
Matches 110; Conservative 69; Mismatches 128; Indels 19; Gaps 6;
QY 3 LEQNQSTDYIEENMGCTDYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMV 62
DB 1 MNATEVDTTQDETVYNSYFYFESMPKPKTEGKAFGEVFLPPLYSLVFLGLFGNSV 60
QY 63 VAIYAYKKQRTKTDVILNAVADLLFTLPFWAVNAVHGWIGKIMCKITSALTYL 122
DB 61 VLVLFKVKRUKSMTDVLNLAISDLLFVLSLPFWGYAADOQVFGGLCKIVSMWLVG 120
QY 123 FVSGMQFLACISIDRYVAVTKV-----PSQSGVGKPCWICFCVWMAAILLSIPQLV 175
DB 121 FYSGIFFIMLSIDRYLAIVHAVFSLKARTLTGV-----ITSLLTWSVAVFASLPGLLF 175
QY 176 ---YTVNDNARCIPFPRLGTSMKALIQMLEI-CIGFVVPFLMGVCFITARTLKM 231
DB 176 STCTENHTYCKTOYS--VNSTTWKVLSSLEINVLGLIPLGIMLFWYSMIIRTLQ 233
QY 232 NIKISRLPKLVLLTVVIVFVITQLPYNIVKFCRAIDIIYSILTSNCKSKRMIDIAIQV 291
DB 234 NEKNRAVRMIFGVVFLFGLFWTPYNNVLFLETL-VELEVLDQCTLERYLDYAIQAT 292
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKV 317
DB 293 GFICHCLNPLIYFELGKFKRYITQL 318
RESULT 11
B55733
G protein-coupled receptor GPR2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C:Accession: B55733
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Helber, M.; Cheng, H.H.Q.; Tsui
Genomics 23, 609-618, 1994
A:Title: Cloning of human genes encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:95154831
A:Accession: B55733
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <MAR>
A:Cross-references: GB:U13667
C:Genetics:
A:Gene: GDB:GPR2
A:Cross-references: GDB:371708; OMIM:600240
A:Map position: 17q21.1-17q21.3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 28.5%; Score 518.5; DB 2; Length 354;
Best Local Similarity 33.9%; Pred. No. 5e-37;
Matches 121; Conservative 65; Mismatches 142; Indels 29; Gaps 7;
QY 12 YIEENMGCTDYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMWVAIY-AYYK 70
DB 5 HYSGDE-EDAYSAPLPELCYKADVQAFSPQSPVSLTVAALGLAGNLVLATHLAARR 63
QY 71 QKRTKTDVILNAVADLLFTLPFWAVNAVHGWIGKIMCKITSALTYLNFVSGMQFL 130
DB 64 AARSPTSAHLQLALADILLALTLPFAAAGALQGSLSATCRTISGLYSASFAGFLFL 123
QY 131 ACISIDRYVAVTKV-----PSQSGVGKPCWICFCVWMAAILLSIPQLVFTVND---NAR 183
DB 124 ACISADRYVAIARALPAGPRPTPCR-AHLVSVIWMLLSLLALLPALLFSQDQREGORR 182

QY	184	CTPIPRYLGTSWKALIOLETCIGFVVPFLINGCVYFIARTLMKNPNIKISRLPKVLL	243
Db	183	CRLLIEPEGLTQVKGSASAVAQVAGFALPLGVMYACVALLGRTLLAARGPERRALRVVV	242
QY	244	TVYIVFIVTQLPVNYIKFCRAIDIIYSLIITSCNNKRMWDIAIQVETSIALFHSCLNPILY	303
Db	243	ALVAAFFVLQLPYSIALLLDADLLAARERSCPAKSKKRDVALLVTSGLALARGCLNPVLY	302
QY	304	VFMGASFKNYVMKVAK-----XGSWRRQRQSVSEFPDSCGTEPTSTFSI	350
Db	303	AFGLGPFPRQDRLRLLRGGSSPGPQRRGCPRRPLS-----SCNAPTTHSL	350

RESULT 12
AS3752
interleukin-8 receptor (clone 5b1a) - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 06-Jan-1995 sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C.Accession: AS3752
R.Prado, C.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava
J. Biol. Chem. 269, 12391-12394, 1994
A.Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A.Reference:

A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-358 <PRA>
A: Cross-references: GB:I24445; NID:q437661; PID:AAA31378.1; PID:q437662
C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor; transmembrane protein

Query Match	28.1%;	Score 511;	DB 2;	Length 358;
Best Local Similarity	32.3%;	Pred. No. 2.2e-36;		
Matches 116; Conservative	72;	Mismatches 139;	Indels 32;	Gaps 8;

Qy	10	DYYEENMGNTYDSQYELI-----CIREVREFAKVLPVFLTFIVFVIGEA	57
Db	8	NYSYE--DFGC--DFSNNYSTDLPTLLDSAPCRSELETNSYVVLIIYI-LVFLSUL	62
Qy	58	GNSMVAIYAYKKQRTKTDVYILNLAVADLLFLPFWAVNAHVGLGKIMKITSIA	117
Db	63	GNSLVMVLVILYSRSTCVTDVYLLNLAIADLLFATLLPIWAASKVHGWTGPTCLCKVSVL	122
Qy	118	LYTLNFGSMQFLACISIDRYAV----TKVPSQSGVGKPCWICFCVWMAAILLSIPQ	172
Db	123	VKEVNFSGILLACISVDRIYLAIVHATRTMIQKRLVK----FICLSMWGVSILSLPI	178
Qy	173	LVFTVNDNARCPIFPYRLGTS---MKALIOMLEICIGVVPFLMGVCYFTARTLMK	229
Db	179	LLFRNAIFPNSSPVCYEDMGNSTAKRWVRLPQTQFGIPLLVMLFCYVFTURTLFQ	238
Qy	230	MPNIKISRPLKVLTVVVIPIVQLPNYVKFCRAIDIIYSLITSNNMSKRMIDIAQVTE	289
Db	239	AHMQQRHARMVFAVVLFLLCWLPYNLVLLTDLMRTHVIOETCERNRNDIDRALDATE	298
Qy	290	SIALFHSLCPILVYFMGSAFKNYMKVAKKGVSNRRQ---RQSVEEFPFDSEGTEPT	345
Db	299	ILGFLSHMLLPYIAFGIKRGYGLGLILAAHGLTSKEFLAKESRPSFVASSSGNTIST	357

RESULT 13
JQ1231
Interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: JQ1231; A46483
R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lym
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: JQ1231; MUID:91376994
A:Accession: JQ1231

A: Molecule type: DNA
A: Residues: 1-355 <BEC>
A: Cross-references: GB:W74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
J: Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
R: Immunol. 148, 1261-1264, 1992
A: Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
A: Reference number: A46483; MUID:92148149
A: Accession: A46483
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-355 <LEE>
A: Cross-references: GB:W82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A: Experimental source: neutrophils
A: Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)
C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.68; Score 501.5; DB 2; Length 355;
Best Local Similarity 33.1%; Pred. No. 1.4e-35;
Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

Query Match	27.6%	Score	501.5	DB 2	Length	355			
Best Local Similarity	33.1%	Pred. No.	1.4e-35						
Matches	107	Conservative	70	Mismatches	127	Indels	19	Gaps	6
Qy	12	YVEENEMNGT-----YDYSOYELICIKEDYREFAKVFELPVFLTIVFVIGLAGNSMVYAI	65						
Db	14	WFEDDFANATGMPPEVKDYS---PCLVVTQTINKYVVV---VYIALVFLLSLGNSLVMLV	68						
Qy	66	YAYYKORTDDVILNLAVADLLLLTLPFWAVNAVHGVGLKMGCKITTSALYTNFVS	125						
Db	69	ILYSKSNRSVTDVYLLNLAMADLLFALTMTPIWAVSKEGWI FGTPCLKVVSLSKVEVFN	128						
Qy	126	GMOFLACISIDRYAV---TKVPSQSGVGKPCWIIICFVNMMAILLIPOLVFTVYVNDNA	182						
Db	129	GILLACISIDRYALAIVHATRTLTQK--RHLVKVFCILGIALSLILSLPFLFRQVFSN	186						
Qy	183	RCIPIFPRYLQ---TSMKALIOLEICIGFVDFPLMGVCYFITARTLMKMPNIKISRPL	239						
Db	187	NSDPVCYEDLGHNTAKRMVWLRIPLPHTFGFILPLLVMFLFCYGTFLRTLFOAHMGQKHRA	246						
Qy	240	KVLLTVIVFIVTQLPYNVKKFCRAIDIIYSLTTSNMKSRMDIAIQVTSIALFHSCLN	299						
Db	247	RVIFAVVLIELLCWLPYNVLLADTLMRTHVIOETCORRNDIDRALDATEILGFLHSCLN	306						
Qy	300	PILYVFNFGASFKNVYMKVAKKYG	322						
Db	307	PIIYAFIGQNFNGFLKMLAARG	329						

RESULT 14
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
R:Federspiel, B.; Melhado, A.M.V.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L
Genomics 16, 707-712, 1993
A>Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a
A:Reference number: A45747; MUID:93315164
A:Accession: A45747
A:Molecule type: mRNA
A:Residues: 1-352 <FED>
A:Cross-references: GB:M92993; NID:g292516; PIDN:AAA16617.1; PID:g292517
R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A>Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl
A:Reference number: A53103; MUID:94103215
A:Accession: A53103
A:Molecule type: mRNA
A:Residues: 1-352 <LOE>
A:Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A>Title: Molecular cloning, characterization, and localization of the human homologue t

A:Reference number: I53006; MUID:93319629

A:Accession: I53006

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <HER>

A:Cross-references: GB:I06797; NID:g414929; PIDN:AAA03209.1; PID:g414928

R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar

Regul. Pept. 47, 247-258, 1993

A:Title: A proposed bovine neurotensin Y (NPY) receptor cDNA clone, or its human homolog

A:Reference number: I59444; MUID:94052833

A:Accession: I59444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <RE2>

A:Cross-references: GB:I01639; NID:g189313; PIDN:AAA16594.1; PID:g189314

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem

A:Reference number: I54751; MUID:94092629

A:Accession: I69203

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <RES>

A:Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869

C:Genetics:

A:Gene: GDB:NPY3R; NPY3

A:Cross-references: GDB:D230002; OMIM:162643

A:Map position: 2q21-2q21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 500.5; DB 2; Length 352;

Best Local Similarity 34.6%; Pred. No. 1.7e-35;

Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENMGTYDYSQVELICIKEDVREFAKVLPVLTIVFVIGLAGNSMVAIYA 67

Db 8 TSDNYTEE---MGSGDYDSMKKEPCFREENAFNFKIFLPTIYSIFLTGIVGNGLVILVMG 64

QY 68 YKKQRTKTDVYILNLAVADLLFTLPWAVNAVHGWLKIMCKITSALYTLNLFVSGM 127

Db 65 YQKLRSMTDKYLHLVSADLLFTLPWAVDAVANWYFGNFKRAVHYITVNLVSSV 124

QY 128 QFLACISIDRYAVTKVPSOSGVGKPC---WIICFCVMAAILLSIPOLVF---NDNA 182

Db 125 LILAFISLDRLAIVHATNSQRPKLLAEKVYVGVWIPALLTIPDFIFANVSEADRY 184

QY 183 RCIPFPYLGTSKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLKVL 242

Db 185 ICDRFYPNDLW---VVFQFHIMVGLILPGVILSCYCIISKLSHSGHQKRAKLT 241

QY 243 LTVVIVPIVQLPYNIVKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSCINPIL 302

Db 242 VILILAFFACWLPYYIGISIDSFILLEIIOGCEFEFENTVHKWISITEALAFFHCCLNPIL 301

QY 303 YVFMGASFK 311

Db 302 YAFGAKFK 310

RESULT 15

S28787

neuropeptide Y/peptide YY receptor Y3 - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999

C:Accession: S28787

R:Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Nestler, E.J.; Duman, R.S.

Mol. Pharmacol. 40, 869-875, 1991

A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.

A:Reference number: S28787; MUID:92100053

A:Accession: S28787

A:Molecule type: mRNA

A:Residues: 1-353 <RIM>

A:Cross-references: EMBL:M86739

C:Superfamily: vertebrate rhodopsin

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 499.5; DB 2; Length 353;

Best Local Similarity 34.5%; Pred. No. 2.1e-35;

Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

QY 13 YEENMGTYDYSQVELICIKEDVREFAKVLPVLTIVFVIGLAGNSMVAIYAYKKQ 72

Db 12 YTEDDL-GSGDYDSMKKEPCFREENAFNRIPLTYISIFLTGIVGNGLVILVMGYQKKL 70

QY 73 RTKTDVYILNLAVADLLFTLPWAVNAVHGWLKIMCKITSALYTLNLFVSGHMOFLAC 132

Db 71 RSMTDKYLHLVSADLLFTLPWAVDAVANWYFGKFLCAVHVITYVNLVSSVLLILAF 130

QY 133 ISIDRYAVTKVPSOSGVGKPC---WIICFCVMAAILLSIPOLVF---YTVNDNARC 184

-Db 131 ISLDRLAIVHATNSQ---KPRKLLAEKVYVGVWLPVALLTIPDLIFADIKEVDERYIC 187

QY 185 IPIFPYLGTSKALIQMLEICIGFVVPFLMGVCYFITARTLMKMPNIKISRPLKVL 244

Db 188 DRFYPSDL---WLNVFQFHIMVGLILPGVILSCYCIISKLSHSGYQKRAKLT 244

QY 245 VVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMEDIAIQVTSIALFHSCINPIL 304

Db 245 LILTFACWLPYYIGISIDSFILLEIIOGCEFEFENTVHKWISITEALAFFHCCLNPIL 304

QY 305 FMGASFK 311

Db 305 FLGAKFK 311

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Job time: 192 sec
